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Supplemental information

B cell genomics behind cross-neutralization of SARS-CoV-2 variants and SARS-CoV

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Subject	Name used in Raw Sequence Files	Gender	Age	COVID Test Result	Days Between Test and Blood Draw	Symptoms	Serum ID50	Serum ID80	RBD ELISA
BG1	DON_1	M	49	positive	48	fever, malaise, chest tightness, loss of smell	655	112	IgG+/IgM+
BG2	DON_2	F	37	positive	36	shortness of breath, chest tightness, loss of smell	0	0	IgG+/IgM-
BG4	DON_4	M	42	positive	50	fever, chills, malaise,	449	99	IgG+/IgM+
BG5	DON_5	M	40	positive	31	n/a	51	0	IgG+/IgM+
BG6	DON_6	M	29	not tested	n/a	cough, malaise, chest tightness, diarrhea, loss of smell, headache	72	24	IgG+/IgM-
BG7	DON_7	M	40	positive	53	loss of smell	155	42	IgG+/IgM+
BG9	DON_9	F	30	positive	51	n/a	74	0	IgG+/IgM-
BG10	DON_10	F	58	positive	42	fever, cough, myalgia and fatigue	255	76	IgG+/IgM-
BG13	DON_13	F	61	not tested	n/a	cough, fever, shortness of breath, rhinitis, nausea/vomitting, diarrhea, loss of smell	77	22	IgG+/IgM+
BG14	DON_14	F	43	positive	59	fever, nausea	68	0	IgG-/IgM+
BG18	DON_18	M	57	positive	60	myalgia, chills, fatigue	353	82	IgG+/IgM+
BG19	DON_19	M	53	positive	61	body aches,fever, fatigue	53	0	IgG+/IgM+
BG20	DON_20	F	40	positive	51	cough, shortness of breath, fever, diarrhea	0	0	IgG+/IgM+
BG21	DON_21	F	50	positive	60	cough, rhinitis, chest tightness, diarrhea, sore throat	0	0	IgG+/IgM+

Table S1. Subject Characteristics, Related to Figure 1 and Figure S1. Shown are the subject IDs, gender, age at time of diagnosis (in years), result of clinical COVID-19 PCR test result, days between the COVID test and blood draw for this study, clinical symptoms at presentation, serum ID50 and ID80 values in a SARS-CoV-2 pseudovirus assay and results in serum ELISA against SARS-CoV-2 RBD. Subjects highlighted in red font were selected for mAb production; n/a = not available.

ISOTYPE	VH GENE	CDR3 HEAVY CHAIN	LIGHT CHAIN	VK/VL GENE	CDR3 LIGHT CHAIN	SORT BAIT	Name	PV IC50 (µg/ml)	PV IG80 (µg/ml)	AV IC50 (µg/ml)	AV IG80 (µg/ml)
IGHM	IGHV6-1	CAKQWLANWFDPW	IGK	IGKV3-20	CQQSESSPYTF	RBD	BG1-1	>50	>50		
IGHG1	IGHV1-8	CARGRAGYYDFWSTSSLDNGGMDVW	IGL	IGLV1-47	CAAWDDSLSGVVF	RBD	BG1-3	>50	>50		
IGHM	IGHV3-23	CVKDVPSMYYIFWSGQGTYW	IGK	IGKV1-5	CQQYNTYSPITF	RBD	BG1-4	>50	>50		
IGHM	IGHV3-23	CAKDLPSRYYDFWSGQGNYW	IGK	IGKV1-5	CQQYNSYSSITF	RBD	BG1-5	>50	>50		
IGHG1	IGHV2-70	CAREMATITGLDYW	IGK	IGKV1-39	CQQSYSTPRTF	RBD	BG1-6	1.178	10.581	0.2037	0.3314
IGHA1	IGHV2-70	CARVPPTDYHFDSW	IGK	IGKV3-20	CQHYGSSPPLTF	2P	BG1-7	>45	>45		
IGHM	IGHV1-18	CARDTSGYRNPGYGMDVW	IGK	IGKV3-11	CQQRSNWPPWTF	2P	BG1-8	>50	>50		
IGHG1	IGHV5-51	CATGTFLAVPGFDFW	IGL	IGLV6-57	CQSYDSGRQGVF	RBD	BG1-9	>25	>25		
IGHM	IGHV3-48	CARDLQRYGSGSSLGPNYFDYW	IGK	IGKV1-9	CQQLDTYPRF	RBD	BG1-10	>50	>50		
IGHM	IGHV4-39	CARRAQYYYDSSGYYDAFDIW	IGK	IGKV3-20	CQQYNSYSTF	RBD	BG1-11	>35	>35		
IGHG1	IGHV3-13	CARDVFRYDSSGRPRYAFDIW	IGK	IGKV2-28	CMQALQTPLTF	RBD	BG1-12	1.151	>50	0.2338	0.3866
IGHG1	IGHV4-59	CARETRWNWIDSW	IGK	IGKV4-1	CQQYHNTPWTF	2P	BG1-13	>30	>30		
IGHG1	IGHV3-53	CARDLVDYGMDVW	IGK	IGKV1-9	CQQLNSYPPYTF	RBD	BG1-14	0.020	0.072	0.03716	0.06751
IGHA1	IGHV3-43D	CAKDGRRDGYNHALDNW	IGK	IGKV1-5	CQQYSSYPTF	RBD	BG1-15	>50	>50		
IGHM	IGHV3-30	CAKGRESTSIGGWFDPW	IGK	IGKV1-16	CQHYNAYPDHL	2P	BG1-16	>37	>37		
IGHM	IGHV2-70	CARTIVGGTNWYFDLW	IGL	IGLV1-44	CASWDDSVNGVF	RBD	BG1-17	24.883	>50	5.174	15.25
IGHM	IGHV4-39	CARRVMGSGWLDSW	IGL	IGLV2-14	CSSYTSSSTWVF	2P	BG1-18	>50	>50		
IGHG1	IGHV3-9	CAKDMGNGFYYYYGLDVW	IGK	IGKV2D-29	CMQTIHLPRVTF	RBD	BG1-19	>30	>30		
IGHA2	IGHV3-23	CAKDAPDVVLVPVPYYHYGLEVW	IGK	IGKV3-20	CQHYGSSRRTF	2P	BG1-20	>50	>50		
IGHA1	IGHV3-30	CARERSGSYYARVELGYW	IGL	IGLV2-14	CSSYTSSITGVF	RBD	BG1-21	>25	>25		
IGHG1	IGHV3-66	CASSRPPIGQLVPGLDLDWFDPW	IGL	IGLV1-40	CQSYDSRLSGWVF	RBD	BG1-22	0.023	0.072	0.09962	0.1181
IGHA1	IGHV3-53	CARDSYRGGGIW	IGK	IGKV1-33	CQQYDNLPQTF	RBD	BG1-23	0.009	0.039	0.02004	0.02348
IGHG1	IGHV1-69	CARGPYYYDSGGYYLDYW	IGK	IGKV3-20	CQQYAGSPRTF	RBD	BG1-24	0.004	0.007	0.04294	0.07228
IGHG1	IGHV3-53	CARDMGGDVFDIW	IGK	IGKV1-9	CQQLNSSPPKLTF	RBD	BG1-25	0.091	0.596	0.1224	0.1401
IGHA1	IGHV4-39	CAAHITVFGIITGNWFDPW	IGL	IGLV1-40	CQSYASSLSVHVVF	RBD	BG1-26	0.360	3.962	0.235	0.3127
IGHA1	IGHV3-53	CARESAAAWGWLDPW	IGK	IGKV1-39	CQQSYSMPYTF	RBD	BG1-27	>40	>40		
IGHG1	IGHV3-23	CAKDLGYSYGSEIFDYW	IGK	IGKV1-39	CQQSYSTPVF	RBD	BG1-28	10.398	39.842	12.75	17.54

ISOTYPE	VH GENE	CDR3 HEAVY CHAIN	LIGHT CHAIN	VK/VL GENE	CDR3 LIGHT CHAIN	SORT BAIT	Name	PV IC50 (µg/ml)	PV IG80 (µg/ml)	AV IC50 (µg/ml)	AV IG80 (µg/ml)
IGHM	IGHV3-30	CARARSGSYYSAIDYW	IGK	IGKV1-33	CQQYDYLPLTF	2P	BG4-1	>50	>50		
IGHM	IGHV3-23	CAKEAYFTAWLHFPFDPW	IGK	IGKV3-20	CQQYGSSLTF	2P	BG4-2	>50	>50		
IGHG3	IGHV3-30	CARDRDDYGDPYGMDVW	IGL	IGLV3-27	CYSVADNMGVF	2P	BG4-3	>50	>50		
IGHG2	IGHV3-15	CTTGPTVRGVSVYW	IGL	IGLV7-46	CLLSYSGAWVF	2P	BG4-4	>50	>50		
IGHG1	IGHV1-2	CARSVGYDAFDVW	IGL	IGLV1-47	CAAWDDSLFVVF	RBD	BG4-5	>45	>45		
IGHM	IGHV3-21	CARDLMDYDILTGYYPAGYW	IGK	IGKV4-1	CQQYFSTPPSTF	RBD	BG4-6	>50	>50		
IGHM	IGHV1-2	CARGPPPPAITMIVVTTVWTS	IGK	IGKV2-28	CMQALQTPYTF	RBD	BG4-7	>35	>35		
IGHG1	IGHV5-10	CARLETTVTTDWFDPW	IGL	IGLV2-14	CSSYTRGNYVF	RBD	BG4-8	>50	>50		
IGHG3	IGHV3-49	CTIGNWHGSGNNIMHDYW	IGK	IGKV4-1	CHQYYLVPFTF	RBD	BG4-9	>50	>50		
IGHG1	IGHV1-2	CARDRWFGKLEGSFDVW	IGL	IGLV2-23	CCSYATGSSVVF	RBD	BG4-10	5.53	48.924	11.48	15.58
IGHM	IGHV4-34	CARDTVVVVGAHAFDIW	IGK	IGKV4-1	CQQYYTTPLTF	RBD	BG4-11	11.335	36.996	10.7	13.55
IGHG1	IGHV4-39	CARPQVLYYYGSGSYSHWFDPW	IGL	IGLV1-40	CQSYDSSLSAVWVF	2P	BG4-12	>50	>50		
IGHM	IGHV3-48	CARGSGWYVGFDYW	IGL	IGLV1-47	CAAWDDSLSALVF	RBD	BG4-13	>50	>50		
IGHM	IGHV1-2	CARVTTIPQYDYGDYYYYYGMDVW	IGL	IGLV2-23	CCSYAGSSTLVF	2P	BG4-14	0.878	8.971	0.2553	0.3563
IGHG3	IGHV4-59	CARDLGQDW	IGK	IGKV3-20	CQQYGSSPWTF	2P	BG4-15	>50	>50		
IGHM	IGHV4-61	CARDIFGSGSPPSGVAFDYW	IGL	IGLV2-14	CSSHTSSSSPHVVF	RBD	BG4-16	0.806	9.388	0.1342	0.1703
IGHG1	IGHV3-53	CARESYGMDVW	IGK	IGKV3-20	CQQYGSSPGTF	2P	BG4-17	0.024	0.102	0.1276	0.2202
IGHG1	IGHV1-69	CARVKEWGSYYSDSGSHGKNYFDYW	IGL	IGLV2-11	CCSYAGTYTVIF	2P	BG4-18	>50	>50		
IGHM	IGHV1-2	CARDGYSSSFIPGPRNYYGMDVW	IGK	IGKV3-15	CQQFNNWPRGTF	RBD	BG4-19	>50	>50		
IGHG1	IGHV1-18	CARPRGRLITFGGLIVTTLDYYYGMGVW	IGK	IGKV2-28	CMQALQTPVTF	2P	BG4-20	>50	>50		
IGHG1	IGHV1-2	CATDKADTSWWEFDPW	IGL	IGLV7-46	CLLSYSGVVVF	RBD	BG4-21	>35	>35		
IGHG1	IGHV3-53	CARFSKLYQWSFDIW	IGL	IGLV2-11	CCSYAGTYTPVVF	2P	BG4-22	>50	>50		
IGHM	IGHV3-53	CARGTHYGSGSYYHW	IGK	IGKV3-15	CQQYNNWPPGLKITF	RBD	BG4-23	>50	>50		
IGHG1	IGHV3-53	CVRDLDYYGMDVW	IGK	IGKV1-9	CQQLNSSPGSLTF	RBD	BG4-24	0.013	0.05	0.02494	0.04633
IGHG1	IGHV3-53	CARDLEVVGAMDVW	IGK	IGKV3-20	CQQYGSPMYTF	2P	BG4-25	0.003	0.013	0.04379	0.0706
IGHG1	IGHV3-53	CAREGPHGMDVW	IGK	IGKV1-33	CQQYDNLPPTF	RBD	BG4-26	0.016	0.072	0.04001	0.05179
IGHG3	IGHV3-53	CARGPVRGVITHFDYW	IGL	IGLV2-14	CSSYTSSSTSSVF	2P	BG4-27	>50	>50		

ISOTYPE	VH GENE	CDR3 HEAVY CHAIN	LIGHT CHAIN	VK/VL GENE	CDR3 LIGHT CHAIN	SORT BAIT	Name	PV IC50 (µg/ml)	PV IG80 (µg/ml)	AV IC50 (µg/ml)	AV IG80 (µg/ml)
IGHD	IGHV3-30	CVKSSSGWYLRLGYW	IGK	IGKV2-28	CMQALQTPTF	2P	BG7-1	>50	>50		
IGHM	IGHV3-53	CAREGRRGQWSWFDPW	IGK	IGKV3-20	CQQFGSSPLYTF	2P	BG7-2	>50	>50		
IGHM	IGHV3-53	CAGSPVRGVITHFDYW	IGL	IGLV2-14	CSSYTSSSTQVF	2P	BG7-3	>50	>50		
IGHM	IGHV4-61	CARVDRRYCIITSCYIFDYW	IGK	IGKV4-1	CQQYYSTPITF	RBD	BG7-4	>50	>50		
IGHM	IGHV3-30	CARGRDGYYYGMDVW	IGK	IGKV1-9	CQQLNSLFTF	2P	BG7-5	>50	>50		
IGHM	IGHV1-2	CARAPPFSSSSIGVDYW	IGK	IGKV1-16	CQQYNSYPLTF	2P	BG7-6	>50	>50		
IGHM	IGHV1-2	CAKDHCATTNCFEYLYFGMGVW	IGK	IGKV2-28	CMQSLQTRTF	2P	BG7-7	>50	>50		
IGHM	IGHV4-4	CARDLTYYGSNGYTNW	IGK	IGKV1-5	CQQYNTYFWTF	2P	BG7-9	>50	>50		
IGHM	IGHV3-53	CASSPVRGVITQFDYW	IGL	IGLV2-14	CSSYTSRSPWVF	2P	BG7-10	>50	>50		
IGHG1	IGHV5-51	CARHDGSKVTTNDYW	IGK	IGKV3-11	CQQRRDWPGTF	2P	BG7-11	>50	>50		
IGHA1	IGHV3-30	CARDRSGSYYRPGYW	IGK	IGKV1-33	CQQYGNLPPLTF	2P	BG7-12	>50	>50		
IGHM	IGHV3-30	CAQTGGSYFGPFDYW	IGL	IGLV2-14	CYSYTTSSTPVVF	2P	BG7-13	>50	>50		
IGHG1	IGHV3-9	CAKDILYGDYVGGFAYW	IGL	IGLV2-14	CSSYTTSSTLVF	RBD	BG7-14	0.385	19.178	0.2084	0.2981
IGHG1	IGHV1-18	CAIPYSSVTFDCW	IGK	IGKV3-20	CQQYGSSRPTF	RBD	BG7-15	0.016	0.092	0.1139	0.1345
IGHG1	IGHV3-53	CARDSQPHYYYGVDVW	IGL	IGLV2-14	CSSYTKTRTLYVF	RBD	BG7-16	3.5992	21.792	3.172	4.817
IGHG1	IGHV5-51	CAKKKDDRAEAVFDYW	IGL	IGLV1-44	CATWDDSLNTYVF	RBD	BG7-17	>50	>50		
IGHG1	IGHV3-53	CARGAAMVKELFDYW	IGK	IGKV4-1	CQQYYSTPLTF	RBD	BG7-18	0.083	0.244	0.1152	0.1601
IGHG1	IGHV3-7	CARVRWLQGGIDYW	IGL	IGLV6-57	CQSYDSGSWVF	RBD	BG7-19	2.735	13.72	1.854	3.653
IGHG1	IGHV1-8	CARGGRYCSSTTCYSGVGMDVW	IGL	IGLV1-40	CQSYDSSLSGWVF	RBD	BG7-20	0.007	0.023	0.05679	0.0942

ISOTYPE	VH GENE	CDR3 HEAVY CHAIN	LIGHT CHAIN	VK/VL GENE	CDR3 LIGHT CHAIN	SORT BAIT	Name	PV IC50 (µg/ml)	PV IG80 (µg/ml)	AV IC50 (µg/ml)	AV IG80 (µg/ml)
IGHM	IGHV3-9	CAKSNSSGLTPFDHW	IGK	IGKV1-39	CQQSYSNPFTF	RBD	BG10-1	>50	>50		
IGHM	IGHV4-39	CARRDGSYFDYW	IGL	IGLV3-1	CQAGDSDTVLF	RBD	BG10-2	>50	>50		
IGHG1	IGHV4-39	CARHVSDGQSIGWLYYFDCW	IGL	IGLV3-21	CQVWDRSSVF	RBD	BG10-3	>50	>50		
IGHA1	IGHV4-31	CARLAPFGERRVDQYYLMDVW	IGK	IGKV2D-29	CMQSTQLPWTF	RBD	BG10-4	>50	>50		
IGHA1	IGHV4-4	CARAYYYYYMDVW	IGL	IGLV1-47	CSAWDDSLRGPVF	RBD	BG10-5	>50	>50		
IGHM	IGHV4-61	CARADRGYCTITDCFIFNYW	IGK	IGKV4-1	CQQYYSTPLTF	RBD	BG10-6	>50	>50		
IGHG1	IGHV3-13	CTRGAHYDFWRGYYTDDHHYMDVW	IGL	IGLV1-40	CQSYDSRLSAWVF	RBD	BG10-7	>50	>50		
IGHA1	IGHV3-11	CVRGEGGPHDAFDIW	IGL	IGLV3-21	CQVWDSSRDLRVF	RBD	BG10-8	>50	>50		
IGHM	IGHV3-7	CVRCGYDDWYFDVW	IGL	IGLV3-1	CQAWDSSTGVF	2P	BG10-9	>50	>50		
IGHG1	IGHV1-8	CGRGPTTAKSGVEWFDPW	IGL	IGLV1-40	CQSFDSSLSGFYVF	RBD	BG10-10	0.099	0.359	0.03891	0.05747
IGHA1	IGHV3-9	CAKDMGWNVFQGLDVW	IGL	IGLV2-14	CTSYRSSSLQGVF	RBD	BG10-11	>50	>50		
IGHA1	IGHV1-18	CARSWSAYYNWFDPW	IGK	IGKV3-20	CQHYGSSPPVTF	2P	BG10-12	>50	>50		
IGHM	IGHV3-15	CTTDRHVRGTYWGAYYYYGMDVW	IGL	IGLV1-44	CAAWDDSLNGLYVF	RBD	BG10-13	>50	>50		
IGHG1	IGHV3-74	CARAVRISSGYGLYGDSDYFDYW	IGL	IGLV3-21	CQVWDSSSDPWVF	2P	BG10-14	12.318	>50	8.683	9.542
IGHM	IGHV3-48	CARARGDAFDIW	IGL	IGLV1-51	CGTWDNSLSVGVF	RBD	BG10-15	>50	>50		
IGHG1	IGHV5-51	CARPLFYCSGGSCLTGYW	IGL	IGLV2-8	CSSYAGSDNWVF	2P	BG10-16	>50	>50		
IGHA1	IGHV3-74	CARGRRDGNDLAPDYW	IGL	IGLV3-10	CYSTDSSDNHRVF	2P	BG10-17	>50	>50		
IGHA1	IGHV3-30	CVKDLGAYASGRLADW	IGK	IGKV1-39	CQQSYTTPYTF	RBD	BG10-18	>50	>50		
IGHG1	IGHV5-51	CARTQWGYNYGSHFFYMDVW	IGL	IGLV1-47	CAAWDASLSGYVF	RBD	BG10-19	0.009	0.026	0.03334	0.03846

Table S2. Selected mAbs for functional evaluation, Related to Figure 2 and Figure S2. Shown are isotype, VH gene, CDRH3 amino acid sequence, light chain kappa or lambda light chain use, V kappa/V lambda gene, light chain CDRL3 amino acid sequence, sorting bait used to identify the cell, mAb name, IC50 in µg/ml in SARS-CoV-2 pseudovirus neutralization assay (PV), IC80 in µg/ml in SARS-CoV-2 pseudovirus neutralization assay, IC50 in µg/ml in SARS-CoV-2 authentic virus neutralization assay (AV), IC80 in µg/ml in SARS-CoV-2 authentic virus neutralization assay for mAbs from subject BG1, BG4, BG7 and BG10 as indicated by the mAb names. All neutralization results in this table are from mAbs expressed as IgG1.

NAME	CoV2 RBD	CoV2 S	CoV RBD	CoV S	MERS RBD	MERS S	Polyreactive	BV Lysate	Neutralizer	Cluster	Isotype	# Mem.
BG1-1	0.231	0.168	0.094	0.064	0.127	0.128	NP	0	0	0	IGHM	5
BG1-3	0.109	0.414	0.099	0.091	0.220	0.162	NP	0	0	0	IGHG1	3
BG1-4	0.098	0.071	0.098	0.081	0.183	0.136	NP	0	0	0	IGHM	3
BG1-5	0.134	0.094	0.244	0.153	0.477	0.183	P	0	0	0	IGHM	3
BG1-6	1.605	1.703	0.108	0.142	0.126	0.079	NP	0	X (G)	4	IGHG1	2
BG1-7	0.120	0.104	0.108	0.086	0.194	0.151	NP	0	0	0	IGHA1	2
BG1-8	0.106	0.126	0.132	0.099	0.270	0.162	NP	0	0	1	IGHM	2
BG1-9	0.139	0.271	0.137	0.092	0.292	0.158	NP	0	0	3	IGHG1	2
BG1-10	0.599	0.461	0.182	0.104	0.379	0.166	NP	0	0	0	IGHM	2
BG1-11	0.092	0.243	0.107	0.100	0.215	0.151	NP	0	0	2	IGHM	2
BG1-12	1.140	0.409	0.086	0.109	0.096	0.067	NP	0	X (G)	0	IGHG1	2
BG1-13	0.118	1.926	0.154	0.566	0.281	1.846	NP	0	0	0	IGHG1	2
BG1-14	1.764	2.528	0.092	0.292	0.101	0.075	NP	0	X (G)	3	IGHG1	2
BG1-15	0.428	0.530	0.101	0.084	0.177	0.127	NP	0	X (mA, dA)	0	IGHA1	2
BG1-16	0.079	0.071	0.066	0.072	0.106	0.103	NP	0	0	0	IGHM	2
BG1-17	1.189	0.686	0.242	0.561	0.387	0.185	NP	0	X (G)	4	IGHM	2
BG1-18	0.200	0.234	0.125	0.090	0.276	0.140	NP	0	0	2	IGHM	2
BG1-19	1.820	1.494	0.137	0.099	0.302	0.241	NP	0	0	0	IGHG1	1
BG1-20	0.105	0.118	0.093	0.087	0.266	0.472	NP	0	0	4	IGHA2	1
BG1-21	0.115	0.140	0.085	0.073	0.165	0.117	NP	0	0	2	IGHA1	1
BG1-22	1.821	2.098	0.300	0.669	0.364	0.174	NP	0	X (G)	4	IGHG1	1
BG1-23	1.239	3.823	0.119	0.638	0.297	0.182	NP	0	X (G, mA, dA)	4	IGHA1	1
BG1-24	1.337	3.552	0.249	0.986	0.417	0.117	P	0	X (G)	3	IGHG1	4
BG1-25	1.121	2.459	0.069	0.205	0.087	0.070	NP	0	X (G)	3	IGHG1	1
BG1-26	1.111	2.351	0.339	0.319	0.086	0.084	NP	0	X (G, mA, dA)	5	IGHA1	2
BG1-27	0.130	0.109	0.158	0.098	0.279	0.222	NP	0	X (mA, dA)	0	IGHA1	1
BG1-28	1.608	2.307	1.577	2.430	0.222	0.227	NP	0	X (G)	3	IGHG1	2

NAME	CoV2 RBD	CoV2 S	CoV RBD	CoV S	MERS RBD	MERS S	Polyreactive	BV Lysate	Neutralizer	Cluster	Isotype	# Mem.
BG4-1	0.081	0.107	0.136	0.078	0.213	0.149	NP	0	0	4	IGHM	11
BG4-2	0.111	0.177	0.159	0.098	0.267	0.195	NP	0	0	2	IGHM	4
BG4-3	0.091	2.136	0.127	0.127	0.234	0.184	NP	0	0	4	IGHG3	3
BG4-4	1.118	0.207	0.176	0.114	0.246	0.196	NP	0	0	3	IGHG2	3
BG4-5	0.388	2.071	0.152	0.089	0.238	0.206	NP	0	0	0	IGHG1	3
BG4-6	0.091	0.103	0.115	0.072	0.180	0.189	NP	0	0	0	IGHM	3
BG4-7	0.065	0.074	0.064	0.060	0.083	0.116	NP	0	0	0	IGHM	3
BG4-8	0.385	1.112	0.105	0.073	0.186	0.157	NP	0	0	3	IGHG1	3
BG4-9	0.188	0.105	0.157	0.080	0.573	0.209	P	0	0	3	IGHG3	2
BG4-10	0.999	1.468	0.197	0.274	0.280	0.207	P	0	X (G)	0	IGHG1	2
BG4-11	1.168	0.666	0.072	0.102	0.110	0.075	NP	0	X (G)	0	IGHM	2
BG4-12	0.168	1.802	0.132	0.110	0.281	0.227	NP	0	0	3	IGHG1	2
BG4-13	0.194	0.242	0.151	0.081	0.320	0.179	NP	0	0	0	IGHM	2
BG4-14	0.297	0.237	0.105	0.159	0.162	0.109	P	0	X (G)	3	IGHM	2
BG4-15	0.112	1.065	0.084	0.226	0.178	0.212	NP	0	0	3	IGHG3	2
BG4-16	1.345	2.671	0.110	0.352	0.142	0.222	NP	0	X (G)	0	IGHM	2
BG4-17	1.552	2.411	0.140	0.275	0.172	0.192	NP	0	X (G)	4	IGHG1	2
BG4-18	0.109	0.645	0.144	0.247	0.632	0.583	P	0	0	0	IGHG1	2
BG4-19	0.135	0.374	0.136	0.094	0.235	0.201	NP	0	0	0	IGHM	2
BG4-20	0.120	0.524	0.173	0.165	0.465	0.472	NP	0	0	3	IGHG1	2
BG4-21	0.983	0.865	0.093	0.080	0.197	0.184	NP	0	0	0	IGHG1	2
BG4-22	0.160	0.169	0.161	0.105	0.248	0.184	NP	0	0	4	IGHG1	1
BG4-23	0.352	1.091	1.085	0.262	2.182	0.730	P	0	0	1	IGHM	1
BG4-24	1.509	2.278	0.152	0.532	0.167	0.186	NP	0	X (G)	3	IGHG1	1
BG4-25	1.098	2.371	0.115	0.392	0.117	0.096	NP	0	X (G)	3	IGHG1	1
BG4-26	1.117	2.461	0.112	0.284	0.102	0.090	NP	0	X (G)	3	IGHG1	1
BG4-27	0.332	1.492	0.284	0.305	0.874	0.522	P	0	0	0	IGHG3	1

NAME	CoV2 RBD	CoV2 S	CoV RBD	CoV S	MERS RBD	MERS S	Polyreactive	BV Lysate	Neutralizer	Cluster	Isotype	# Mem.
BG7-1	0.120	0.093	0.115	0.103	0.389	0.885	P	0	0	5	IGHD	12
BG7-2	0.098	0.078	0.078	0.078	0.124	0.167	NP	0	0	0	IGHM	9
BG7-3	0.111	0.089	0.103	0.093	0.282	0.463	NP	0	0	0	IGHM	9
BG7-4	0.111	0.102	0.095	0.087	0.161	0.262	NP	0	0	1	IGHM	6
BG7-5	0.104	0.097	0.092	0.080	0.149	0.161	NP	0	0	5	IGHM	5
BG7-6	0.115	0.104	0.106	0.095	0.223	0.197	NP	0	0	0	IGHM	3
BG7-7	0.121	0.104	0.098	0.084	0.198	0.283	NP	0	0	0	IGHM	3
BG7-9	0.137	0.101	0.105	0.082	0.141	0.195	NP	0	0	0	IGHM	2
BG7-10	0.117	0.096	0.109	0.116	0.415	0.490	NP	0	0	0	IGHM	2
BG7-11	0.150	0.095	0.085	0.086	0.118	0.143	NP	0	0	0	IGHG1	2
BG7-12	0.101	0.077	0.082	0.078	0.122	0.194	NP	0	0	3	IGHA1	2
BG7-13	0.124	0.088	0.082	0.093	0.218	0.421	NP	0	0	4	IGHM	2
BG7-14	1.456	1.448	0.116	0.281	0.164	0.065	NP	0	X (G)	4	IGHG1	1
BG7-15	1.500	1.729	0.170	0.444	0.225	0.091	NP	0	X (G)	4	IGHG1	1
BG7-16	0.653	0.880	0.084	0.647	0.143	0.118	NP	0	X (G)	0	IGHG1	1
BG7-17	0.112	0.092	0.077	0.080	0.129	0.175	NP	0	0	0	IGHG1	1
BG7-18	1.074	0.930	0.075	0.447	0.115	0.065	NP	0	X (G)	3	IGHG1	1
BG7-19	1.068	0.942	0.181	0.212	0.092	0.064	NP	0	X (G)	4	IGHG1	1
BG7-20	1.781	1.193	0.118	0.449	0.127	0.094	NP	0	X (G)	3	IGHG1	1

NAME	CoV2 RBD	CoV2 S	CoV RBD	CoV S	MERS RBD	MERS S	Polyreactive	BV Lysate	Neutralizer	Cluster	Isotype	# Mem.
BG10-1	0.595	0.442	0.148	0.073	0.268	0.196	NP	0	0	0	IGHM	36
BG10-2	0.478	0.226	0.203	0.069	0.276	0.184	NP	0	0	0	IGHM	15
BG10-3	0.392	0.907	0.085	0.087	0.137	0.153	NP	0	0	0	IGHG1	9
BG10-4	0.323	0.748	0.093	0.066	0.136	0.150	NP	0	X (mA, dA)	0	IGHA1	9
BG10-5	0.145	0.101	0.097	0.067	0.165	0.140	NP	0	X (dA)	0	IGHA1	8
BG10-6	0.212	0.135	0.123	0.072	0.178	0.159	NP	0	0	2	IGHM	6
BG10-7	0.189	0.234	0.096	0.077	0.229	0.173	P	0	0	0	IGHG1	6
BG10-8	0.546	0.642	0.105	0.068	0.130	0.141	NP	0	X (mA, dA)	0	IGHA1	5
BG10-9	0.161	0.137	0.158	0.084	0.265	0.207	NP	0	0	0	IGHM	5
BG10-10	1.615	1.880	0.092	0.152	0.089	0.066	NP	0	X (G)	3	IGHG1	4
BG10-11	0.759	1.076	0.072	0.073	0.106	0.124	NP	0	X (mA, dA)	0	IGHA1	3
BG10-12	0.423	0.213	0.149	0.143	0.268	0.372	NP	0	0	0	IGHA1	2
BG10-13	0.633	0.372	0.221	0.105	0.518	0.651	P	0	0	5	IGHM	2
BG10-14	1.856	1.996	0.208	1.032	0.098	0.083	NP	0	X (G)	0	IGHG1	2
BG10-15	0.199	0.132	0.087	0.064	0.129	0.130	NP	0	0	2	IGHM	2
BG10-16	0.264	0.551	0.090	0.101	0.182	0.313	NP	0	0	0	IGHG1	2
BG10-17	0.276	0.155	0.094	0.066	0.130	0.133	NP	0	0	0	IGHA1	2
BG10-18	0.564	0.852	0.138	0.118	0.389	0.651	NP	0	0	0	IGHA1	2
BG10-19	2.075	1.956	2.037	3.323	0.146	0.613	NP	0	X (G)	4	IGHG1	2
mGO53	0.111	0.121	0.100	0.072	0.197	0.179	NP	n/a	n/a	n/a		
3B12	n/a	n/a	0.119	0.979	2.181	2.325	n/a	n/a	n/a	n/a		
S227.14	n/a	n/a	2.338	3.279	0.455	1.354	n/a	n/a	n/a	n/a		
NIH45-46	n/a	n/a	n/a	n/a	n/a	n/a	n/a	X	n/a	n/a		
45-46m2	n/a	n/a	n/a	n/a	n/a	n/a	n/a	X	n/a	n/a		
3BNC117	n/a	n/a	n/a	n/a	n/a	n/a	n/a	0	n/a	n/a		

Table S3. mAb Binding to SARS-CoV-2 S trimer and RBD, related to Figures 2, 4 and Figure S2. Heat map summarizing the area under the curve (AUC) values from ELISAs testing for binding to SARS-CoV-2, SARS-CoV and MERS-CoV RBD and S trimer respectively. Shown are also mAb polyreactivity as defined by binding to at least two of the four antigens ssDNA, dsDNA, LPS or insulin (**STAR Methods**), mAb reactivity in a baculovirus (BV) lysate assay (**STAR Methods**), SARS-CoV-2 neutralizer status, TC and isotype of the cell of origin and the number of clonal members for mAbs from BG1, BG4, BG7 and BG10. Red fields indicate high binding in ELISA (AUC > 1), orange fields intermediate binding (AUC 0.25-1) and white fields low or non-detectable binding (AUC < 0.25). (P) indicates polyreactive mAbs, (NP) indicates non-polyreactive mAbs, (X) indicates presence and (0) absence of reactivity in BV lysate assay or neutralizing activity in SARS-CoV-2 pseudovirus assay as indicated. When neutralizing activity was detected, the neutralizing form of the mAb (IgG (G), monomeric IgA (mA) or dimeric IgA (dA)) is indicated (**Figure S2J, Table S2**). mGO53 = negative control mAb (Wardemann et al., 2003), 3B12 = positive control mAb for MERS-CoV S and MERS-CoV RBD (Tang et al., 2014), S227.14 = positive control mAb for SARS-CoV S and SARS-CoV RBD (Rockx et al., 2008), NIH45-46 (Scheid et al., 2011) and 45-46m2 (Diskin et al., 2013) are positive control mAbs and 3BNC117 (Scheid et al., 2011) a negative control mAb for the baculovirus lysate assay (**STAR Methods**).

Gene	Cluster	avg_logFC	p_val_adj
EMP3	0	0.742674423	7.3546E-231
CIB1	0	0.704189386	5.3201E-174
LITAF	0	0.696585826	1.1097E-144
LGALS1	0	0.648787158	6.46448E-87
RHOB	0	0.591642578	1.06238E-85
COTL1	0	0.586451155	4.6413E-187
SRGN	0	0.570442148	3.10905E-24
PSAP	0	0.528844098	6.22108E-96
YWHAH	0	0.52011957	1.77468E-44
TNFRSF1B	0	0.510460172	6.21712E-57
ITM2C	0	0.509568003	1.57423E-77
IFITM2	0	0.450464045	9.90654E-88
FCRLA	0	0.444860614	1.76974E-91
SYK	0	0.43620199	1.16462E-85
THEMIS2	0	0.402880483	1.43292E-83
VOPP1	0	0.401409487	6.66506E-78
CNFN	0	0.387880767	2.94301E-19
S100A6	0	0.385589924	1.87186E-38
CBLB	0	0.384918125	1.32423E-81
RGS2	0	0.381306354	1.48402E-47
GPR183	0	0.380304968	2.76209E-66
NEAT1	0	0.379959446	4.51826E-59
KLK1	0	0.373715288	5.24563E-20
LY6E	0	0.368067023	7.06007E-75
MAP1LC3B	0	0.36352458	4.2152E-38
CLECL1	0	0.359971797	4.61598E-21
ARL4C	0	0.359298389	8.05691E-19
FCGR2B	0	0.359256692	1.82238E-75
ENC1	0	0.357722215	2.84402E-59
MYADM	1	1.243403044	2.2593E-225
TCL1A	1	1.225934628	3.7055E-199
IGLL5	1	1.046009213	2.42295E-69
TUBA1A	1	1.035589682	2.7488E-164
BACH2	1	0.901778359	1.0079E-144
CXCR4	1	0.864937509	8.8657E-189
FCER2	1	0.827531376	8.03565E-86
CA5B	1	0.783617366	9.15507E-76
FOS	1	0.762212908	1.6744E-99
YBX3	1	0.739249717	4.63058E-44
TAGAP	1	0.705203585	4.6411E-109
TSC22D3	1	0.700201233	2.1628E-176
TXNIP	1	0.68403341	5.6806E-154
IQGAP1	1	0.682830487	8.1883E-82
ITM2B	1	0.682475362	1.6985E-113
IL4R	1	0.673832661	1.01944E-36
CFAP20	1	0.669235711	6.18216E-48
PIK3IP1	1	0.666654627	5.61513E-36
APLP2	1	0.602007836	3.22075E-48
DUSP1	1	0.601203282	6.7298E-111
ARL4A	1	0.57224004	7.75837E-46
FOXP1	1	0.559891381	1.368E-105
SNX9	1	0.550918925	2.06177E-56
FAM129C	1	0.54710977	2.79768E-55
KLF3	1	0.541580676	2.59724E-32
SNX29	1	0.530698011	5.19794E-35
JUN	1	0.514755136	7.63325E-56
TMEM123	1	0.510120702	3.91958E-29
H1FX	1	0.507777606	1.97836E-11
LINC00926	1	0.495411334	2.60423E-63
LINC01857	2	0.89658002	6.2496E-141
LY9	2	0.805186669	1.05659E-55
ZNF331	2	0.793353573	1.2954E-112
NR4A2	2	0.716041154	8.47331E-46
ZFP36	2	0.683501728	8.90518E-92
JUNB	2	0.621795691	5.86253E-87
CXCR4	2	0.612559872	3.1113E-119
H3F3B	2	0.539599702	4.44893E-84
RGS2	2	0.48301966	2.17516E-31
SELENOK	2	0.449154225	1.36643E-49
CD83	2	0.437254403	1.85206E-45
SAT1	2	0.429318869	2.81184E-36
BTG1	2	0.421039343	6.36178E-76
EZR	2	0.415966914	7.77817E-86
IDI1	2	0.411111698	1.24088E-23
HSPA5	2	0.401979123	3.28919E-29
FTH1	2	0.397221901	1.29557E-58
C7orf50	2	0.388294498	6.36042E-20
ZFP36L2	2	0.376235895	1.64603E-23
ATP6V0C	2	0.363370498	3.383E-34
PTP4A1	2	0.356090768	4.39288E-16
GPR183	2	0.350688212	1.5168E-24
SELENOM	2	0.347282859	1.93383E-07
RPS3	2	0.334120925	3.2167E-182
PDCD4	2	0.333819409	2.21968E-18
PDE4B	2	0.328614506	8.83776E-26
DDIT4	2	0.328235507	5.38612E-06
RPL3	2	0.325632471	8.4784E-151
ZFAS1	2	0.322384422	3.30755E-41
SNX9	2	0.322189434	2.42412E-32

Gene	Cluster	avg_logFC	p_val_adj
PDE4D	3	0.617391009	1.397E-74
GRAMD1C	3	0.543300334	7.13152E-80
TMEM156	3	0.482190051	2.26558E-75
NFKBIA	3	0.404665782	4.09009E-61
CXCR3	3	0.390844162	1.47343E-37
CFLAR	3	0.346347436	7.7557E-37
PIM3	3	0.331141279	5.80545E-32
TKT	3	0.328569406	3.22016E-51
CD70	3	0.315320672	1.15173E-18
RHOF	3	0.312104151	2.00606E-29
MGAT4A	3	0.304846784	1.50606E-26
HOPX	3	0.298667192	3.66945E-23
CAPG	3	0.296711301	1.13313E-45
MARCKSL1	3	0.295156785	1.35421E-35
S100A10	3	0.289820808	7.31663E-59
CD80	3	0.285129407	1.57037E-19
ZFP36L1	3	0.282469669	3.44486E-27
COCH	3	0.280678468	1.25073E-25
HMGA1	3	0.279838593	9.79584E-37
FAS	3	0.275149572	2.2978E-11
BASP1	3	0.27404004	6.04891E-23
PAPSS1	3	0.261811155	1.77194E-19
ITGB2-AS1	3	0.258236248	4.32595E-23
LYPLAL1	3	0.258036742	1.67183E-18
NME2	3	0.256528086	7.03615E-27
MIF	3	0.253228431	2.94818E-27
LMNA	3	0.252636567	6.56549E-15
ACTG1	4	2.187488961	0
GAPDH	4	1.415694495	0
S100A10	4	1.383357144	7.1989E-274
ACTB	4	1.24345584	0
TKT	4	1.199748144	1.9806E-301
PFN1	4	1.19354296	0
CORO1A	4	1.132533451	0
HSPA8	4	1.082110641	3.1929E-263
S100A4	4	1.056014677	3.5839E-181
HMGA1	4	1.043888335	1.766E-253
CNN2	4	1.042657878	3.5596E-276
SELL	4	1.018082894	5.36E-218
TMSB10	4	0.991661677	0
ARPC1B	4	0.991292639	4.6721E-219
CLIC1	4	0.952470509	6.7659E-232
RAC2	4	0.938413504	1.1682E-246
ARHGDIB	4	0.903029757	1.3383E-289
SLC25A5	4	0.889602921	6.0617E-229
VIM	4	0.859557756	7.6166E-175
PPP1R18	4	0.840569512	1.9298E-201
PPP1CA	4	0.833400583	3.9625E-215
CAPZB	4	0.814333233	3.7553E-206
ANXA2	4	0.803901635	2.6824E-162
CAPG	4	0.793993669	6.5753E-194
CFL1	4	0.778148295	1.4072E-279
LDHB	4	0.752416695	7.1978E-191
LTB	4	0.736496549	1.6201E-162
TUBB	4	0.725367271	1.0133E-110
PPIA	4	0.721525054	1.9377E-250
LCP1	4	0.719491241	1.6389E-135
PTPRC	5	1.302366222	3.49668E-69
MALAT1	5	1.15555907	9.4795E-118
TMEM123	5	1.080549661	0.000248819
B4GALT1	5	1.077234784	3.41559E-24
NFKBID	5	1.057845136	7.31809E-09
CEMIP2	5	1.021712697	2.23084E-06
LINC00926	5	1.016310566	7.83723E-33
VPS13C	5	1.015256821	0.003396168
MTRNR2L12	5	1.012070633	7.29679E-48
SMCHD1	5	1.001589673	2.43245E-26
NSF	5	0.997369196	1.08153E-09
BACH1	5	0.983250651	1.45033E-12
PARP14	5	0.975468976	3.06721E-05
EML4	5	0.971647618	1.40649E-31
CD69	5	0.967358368	0.00044358
CASP8	5	0.954006026	1.85909E-11
BTG2	5	0.953929298	3.32066E-09
NCOA3	5	0.949408248	7.56379E-17
SF1	5	0.949164446	4.29637E-55
REL	5	0.941261525	1.25707E-27
MS4A1	5	0.940841015	1.15489E-49
AKAP13	5	0.936896357	3.64942E-06
TMEM131L	5	0.931662294	0.000401935
PRDM2	5	0.921624785	7.82581E-18
PNN	5	0.918617999	6.30035E-23
STK4	5	0.914263461	1.75642E-21
PELI1	5	0.902929851	0.000182649
SRSF4	5	0.899508387	2.23408E-07

Table S4. Transcriptome cluster marker genes, Related to Figure 4 and Figure S4. For each of the 6 transcriptome clusters the top 30 genes that are differentially upregulated are displayed. Genes are included only if their minimum log fold change is greater than 0.25 with a false discovery rate (FDR) < 0.05. Columns show the gene name, transcriptome cluster, average log fold change (avg_logFC) and BH adjusted P values (p_val_adj) respectively.

	BG10-19 Fab SARS-CoV-2 S 6P	BG1-22 Fab SARS-CoV-2 S 6P	BG7-15 Fab SARS-CoV-2 S 6P	BG7-20 Fab SARS-CoV-2 S 6P	BG1-24 Fab SARS-CoV-2 S 6P
PDB	**7M6E**	**7M6F**	**7M6G**	**7M6H**	**7M6I**
EMD	**23693**	**23694**	**23695**	**23696**	**23697**
Data collection conditions					
Microscope	Talos Arctica	Talos Artica	Talos Arctica	Talos Artica	Talos Artica
Camera	Gatan K3 Summit	Gatan K3 Summit	Gatan K3 Summit	Gatan K3 Summit	Gatan K3 Summit
Magnification	45,000x	45,000x	45,000x	45,000x	45,000x
Voltage (kV)	200	200	200	200	200
Recording mode	counting	counting	counting	counting	counting
Dose rate (e^-/pixel/s)	13.5	13.3	13.8	13.8	13.3
Electron dose ($e^-/Å^2$)	60	60	60	60	60
Defocus range (μm)	0.7 – 2.0	0.7 – 2.0	0.7 – 2.0	0.7 – 2.0	0.7 – 2.0
Pixel size (Å)	0.8689	0.8689	0.8689	0.8689	0.8689
Micrographs collected	3,807	3,386	3,065	3,717	2,609
Micrographs used	2,860	2,720	2,464	2,830	2,060
Total extracted particles	856,326	756,649	791,968	809,834	556,346
Refined particles	162,522	188,436	209,924	230,863	105,245
Particles in final refinement	101,085	71,104	130,297	135,666	84,059
Symmetry imposed	C3	C1	C1	C1	C1
Nominal Resolution (Å)					
FSC 0.5 (unmasked/masked)	7.5/3.7	7.6/4.1	7.8/4.0	8.0/4.3	8.3/4.5
FSC 0.143 (unmasked/masked)	4.4/3.3	5.9/3.9	5.2/3.7	6.7/3.8	6.7/4.0
Refinement and Validation					
Initial model used	7K43	7K4N	6XKL	6XKL	6XKL
Number of atoms					
Protein	28,466	27,798	25,662	25,238	28,871
Ligand	715	873	837	675	779
MapCC (global/local)	0.81/0.79	0.80/0.75	0.74/0.73	0.79/0.76	0.86/0.81
Map sharpening B-factor	55.7	75.3	80.7	92.4	79.1
R.m.s. deviations					
Bond lengths (Å)	0.002	0.005	0.01	0.015	0.001
Bond angles (°)	0.6	0.89	0.92	0.73	0.9
MolProbity score	2.37	2.26	2.46	2.19	2.14
Clashscore (all atom)	19.7	14.8	18.1	19.24	15.2
Poor rotamers (%)	1.3	1.1	2.4	0.32	0
Ramachandran plot					
Favored (%)	94	97.2	93.7	96.6	92.9
Allowed (%)	5.6	2.8	6.3	3.2	6.5
Disallowed (%)	0.4	0	0	0.2	0.6

Table S5. Cryo-EM data collection and refinement statistics, Related to Figures 3, 5, and 6.

	BG4-25 - SARS2-RBD *(12-2, SSRL)*
PDB ID	**7M6D**
Data collection[a]	
Space group	$P2_12_12_1$
Unit cell (Å)	56.0, 104.3, 268.8
α, β, γ (°)	90, 90, 90
Wavelength (Å)	0.979
Resolution (Å)	38.8-3.0 (3.16-3.0)
Unique Reflections	31,903 (4079)
Completeness (%)	97.9 (88.1)
Redundancy	6.1 (4.2)
$CC_{1/2}$ (%)	97.2 (25.9)
$\langle I/\sigma I \rangle$	4.0 (0.7)
Mosaicity (°)	0.23
R_{merge} (%)	27.1 (135.8)
R_{pim} (%)	12.5 (88.6)
Wilson *B*-factor	60.9
Refinement and Validation	
Resolution (Å)	38.8 - 3.1
Number of atoms	
Protein	8,183
Ligand	60
Waters	0
R_{work}/R_{free} (%)	21.5/26.2
R.m.s. deviations	
Bond lengths (Å)	0.01
Bond angles (°)	1.6
MolProbity score	1.89
Clashscore (all atom)	18.9
Poor rotamers (%)	0.9
Ramachandran plot	
Favored (%)	94.7
Allowed (%)	5.3
Disallowed (%)	0
Average *B*-factor (Å)	73.5

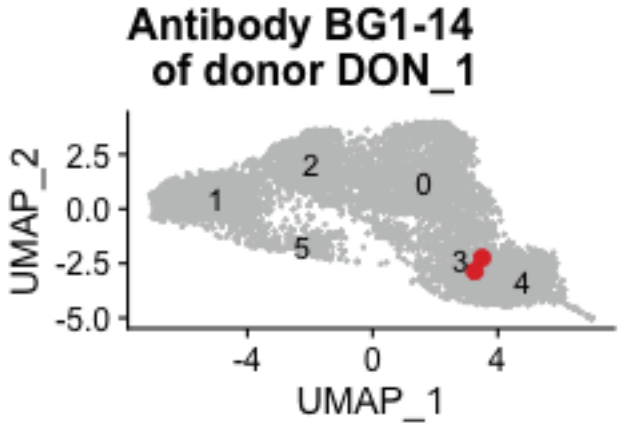
[a]Numbers in parentheses correspond to the highest resolution shell

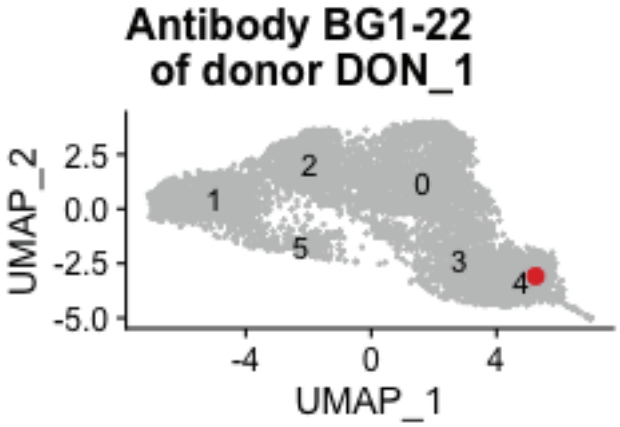
Table S6. X-ray data collection and refinement statistics, Related to Figure 5.

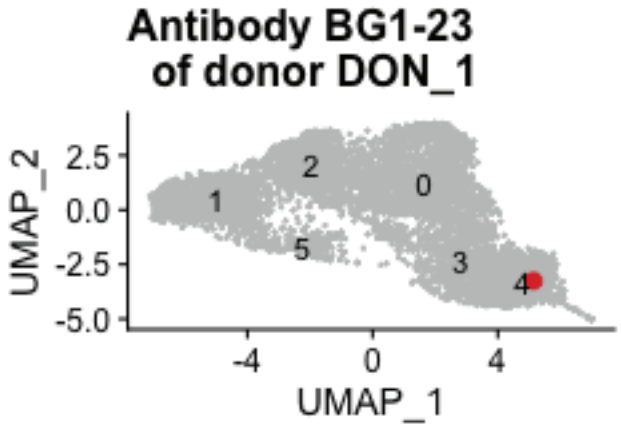
Data S1 (includes this page and the following 15 pages), Related to Figure 4 and Tables S2 and S3. UMAP plots displaying clonal members of all validated mAbs (Tables S2 and S3). Each plot represents where the tested mAb along with its clonally related cells are mapped on the transcriptome landscape.

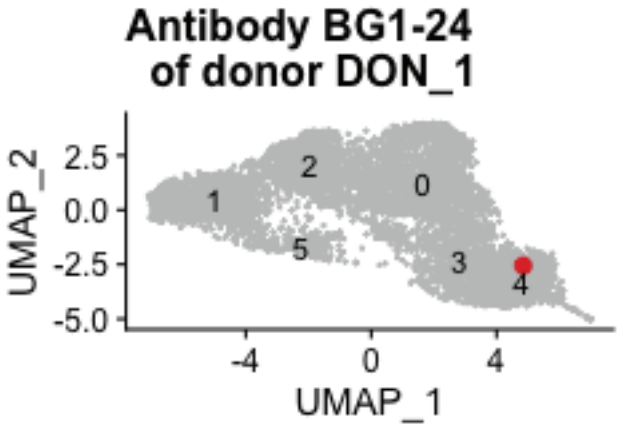
Clones of the tested antibodies

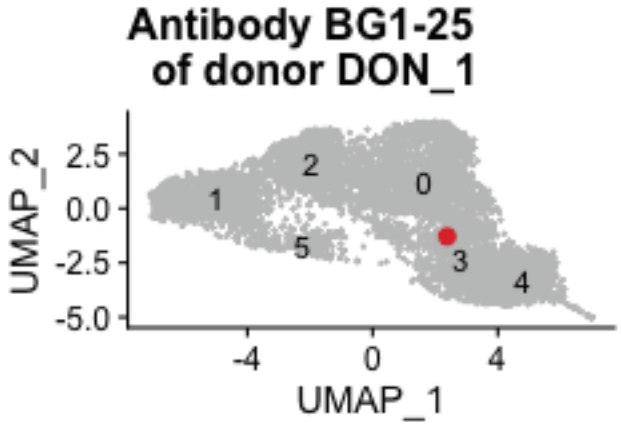
Potently Neutralizing Antibodies










Antibody BG1-25
of donor DON_1
UMAP_2
UMAP_1
2.5
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-5.0
-4
0
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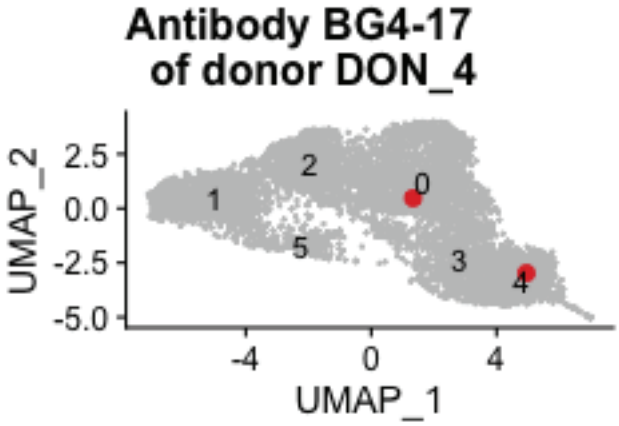
1
2
3
4
5


Antibody BG4-17
of donor DON_4
UMAP_2
UMAP_1
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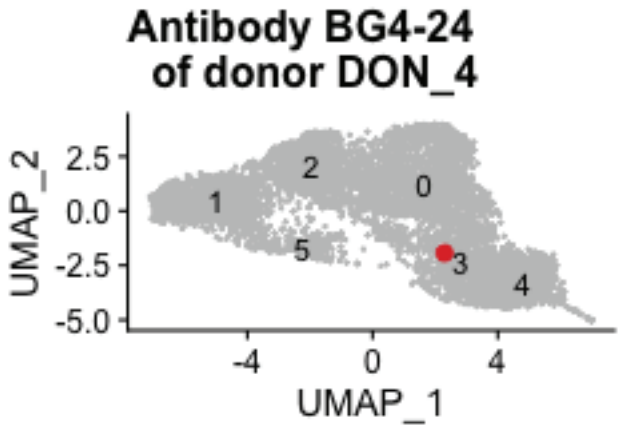
-5.0
-4
0
4
0
1
2
3
4
5


Antibody BG4-24
of donor DON_4
UMAP_2
UMAP_1
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-5.0
-4
0
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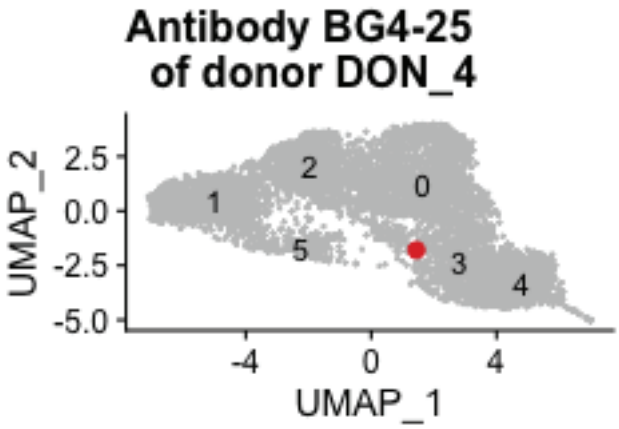
0
1
2
3
4
5


Antibody BG4-25
of donor DON_4
UMAP_2
UMAP_1
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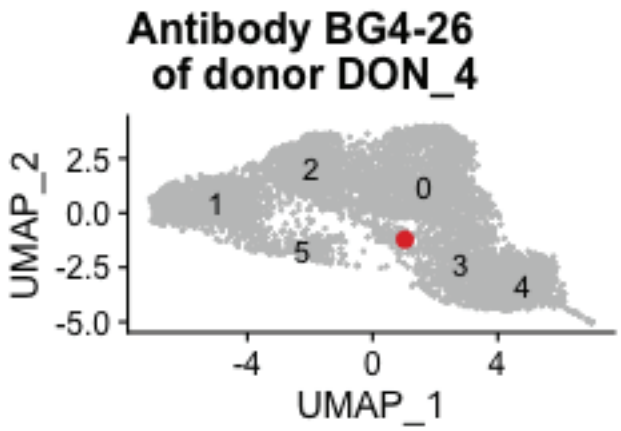
0.0
-2.5
-5.0
-4
0
4
0
1
2
3
4
5


Antibody BG4-26
of donor DON_4
UMAP_2
UMAP_1
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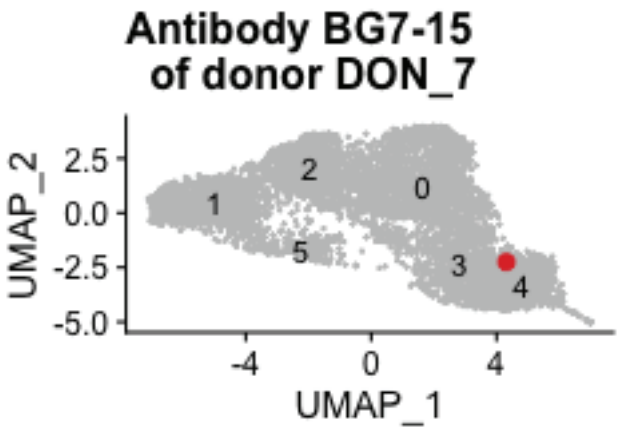
-5.0
-4
0
4
0
1
2
3
4
5


Antibody BG7-15
of donor DON_7
UMAP_2
UMAP_1
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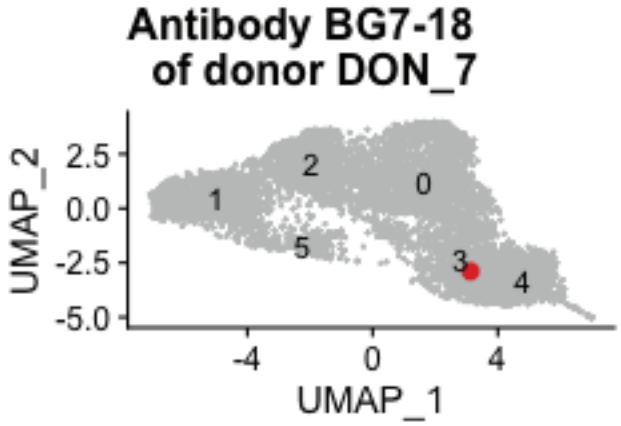
-2.5
-5.0
-4
0
4
0
1
2
3
4
5


Antibody BG7-18
of donor DON_7
UMAP_2
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0.0
-2.5
-5.0
-4
0
4
UMAP_1
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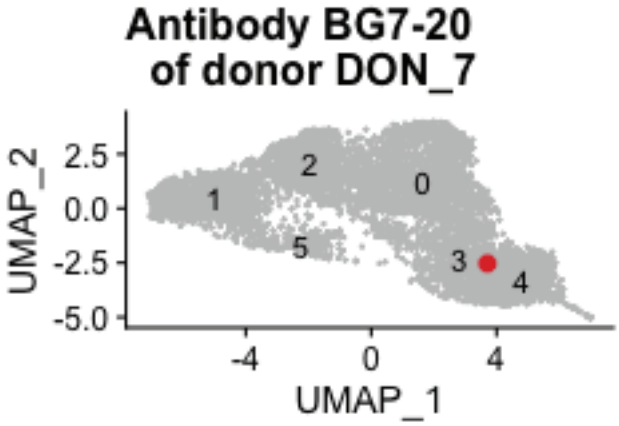
1
2
3
4
5


Antibody BG7-20
of donor DON_7
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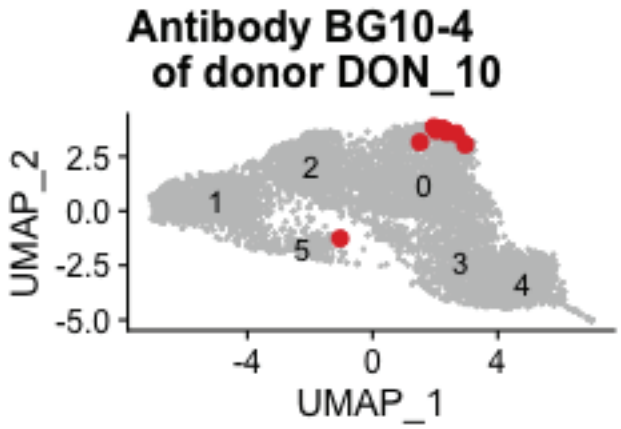
-2.5
-5.0
-4
0
4
UMAP_1
0
1
2
3
4
5


Antibody BG10-4
of donor DON_10
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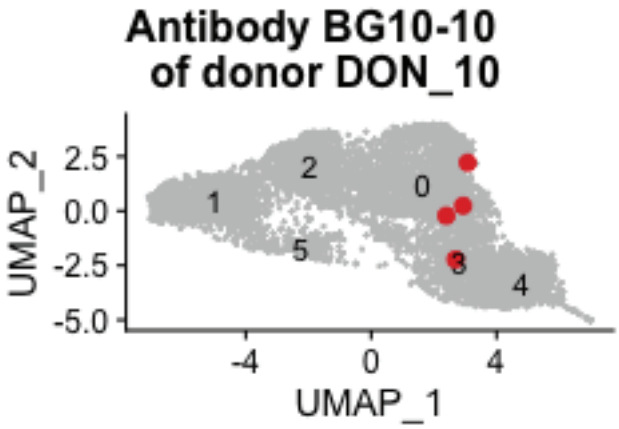
-5.0
-4
0
4
UMAP_1
0
1
2
3
4
5


Antibody BG10-10
of donor DON_10
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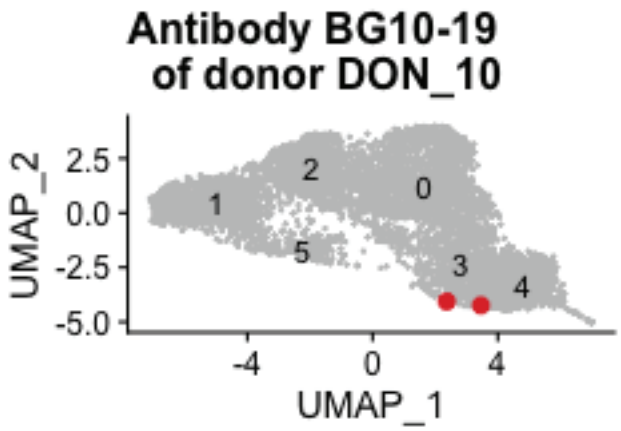
-5.0
-4
0
4
UMAP_1
0
1
2
3
4
5


Antibody BG10-19
of donor DON_10
UMAP_2
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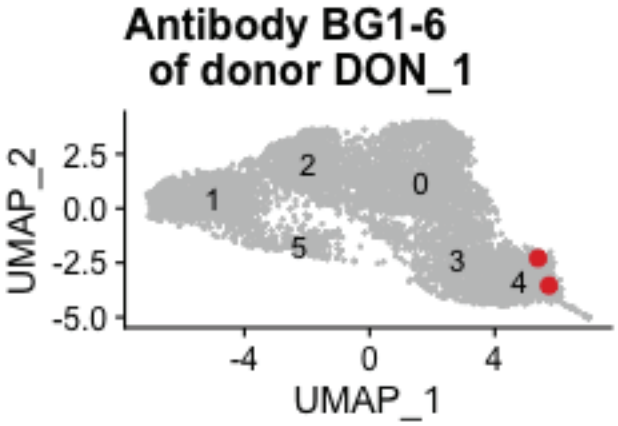
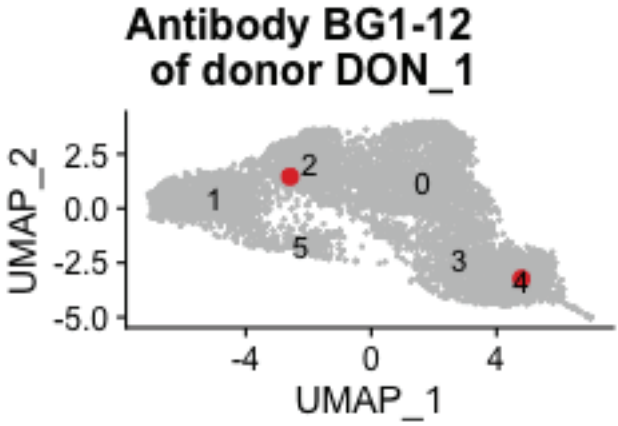
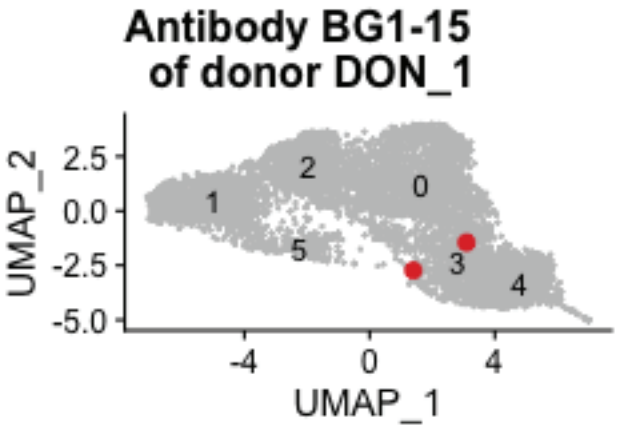
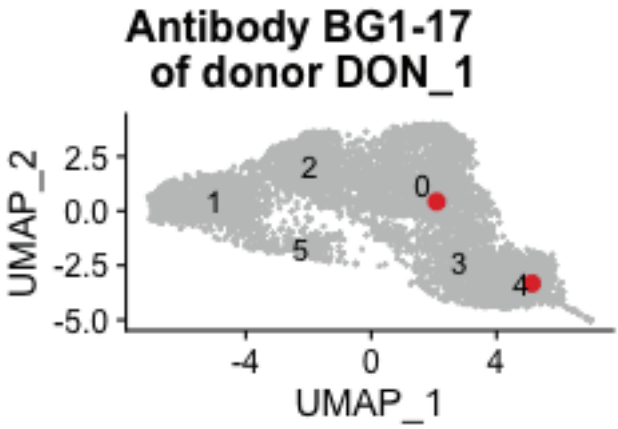
-5.0
-4
0
4
UMAP_1
0
1
2
3
4
5

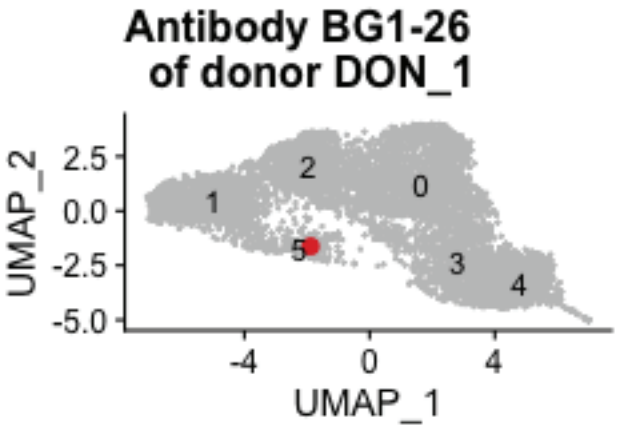
Low Neutralizing Antibodies

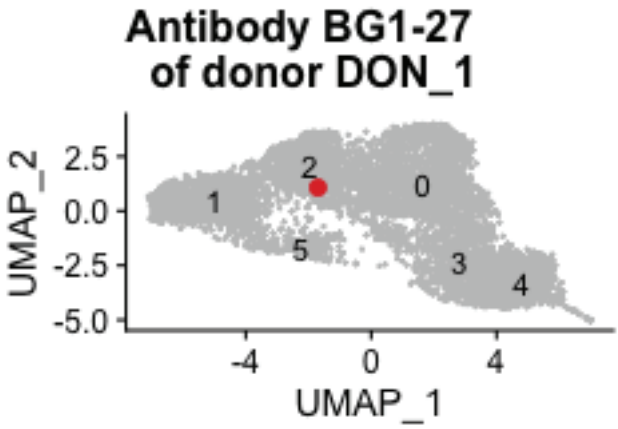


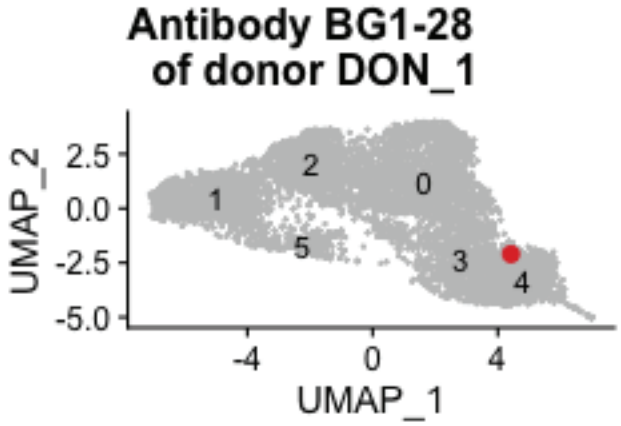











Antibody BG1-28
of donor DON_1
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UMAP_1
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-5.0
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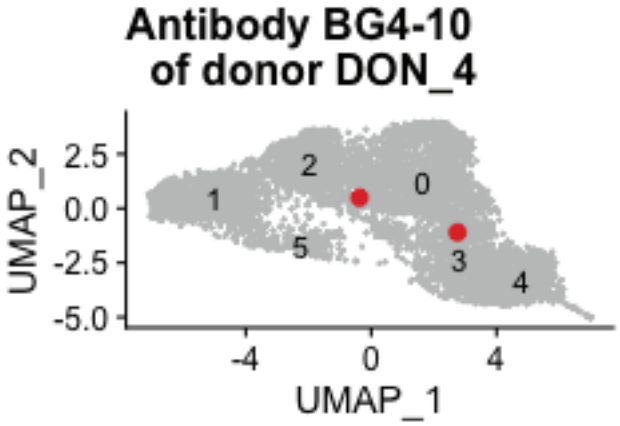
1
2
3
4
5


Antibody BG4-10
of donor DON_4
UMAP_2
UMAP_1
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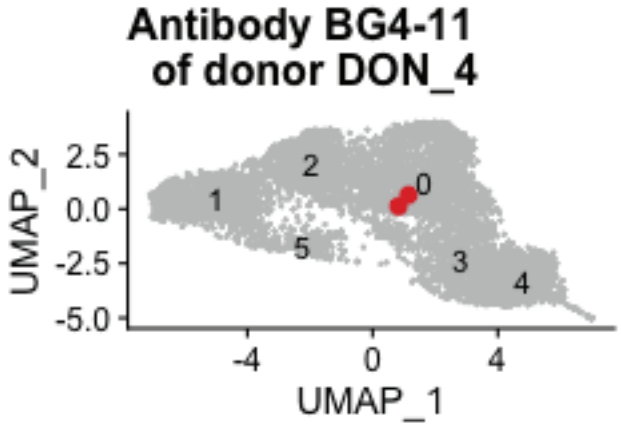
-2.5
-5.0
-4
0
4
0
1
2
3
4
5


Antibody BG4-11
of donor DON_4
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UMAP_1
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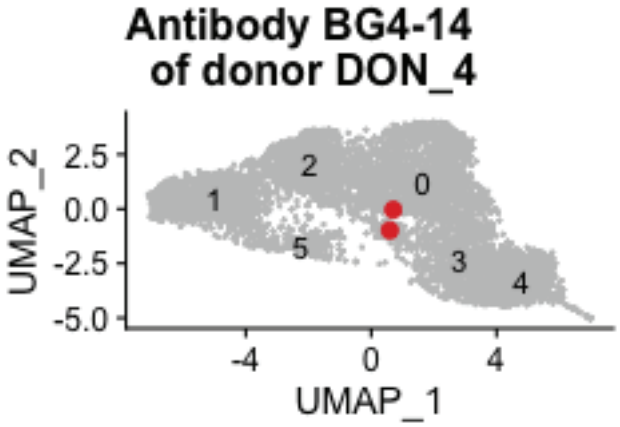
4
5


Antibody BG4-14
of donor DON_4
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UMAP_1
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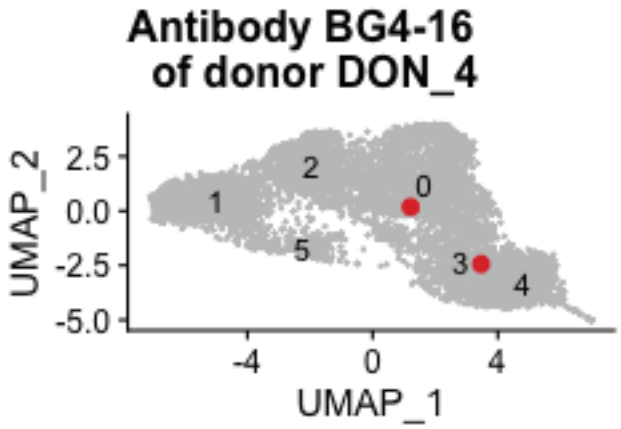
2
3
4
5


Antibody BG4-16
of donor DON_4
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UMAP_1
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-5.0
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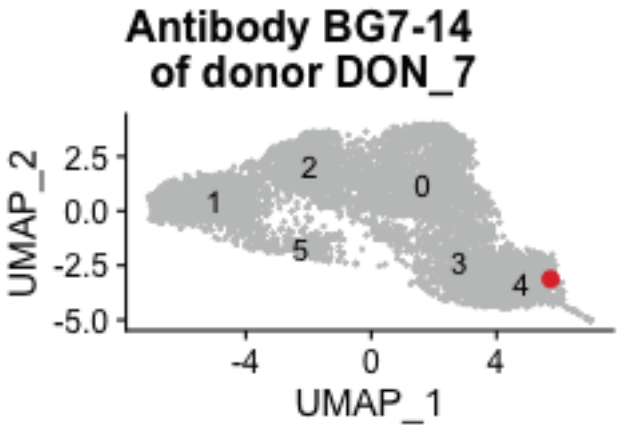
4
5


Antibody BG7-14
of donor DON_7
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UMAP_1
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-2.5
-5.0
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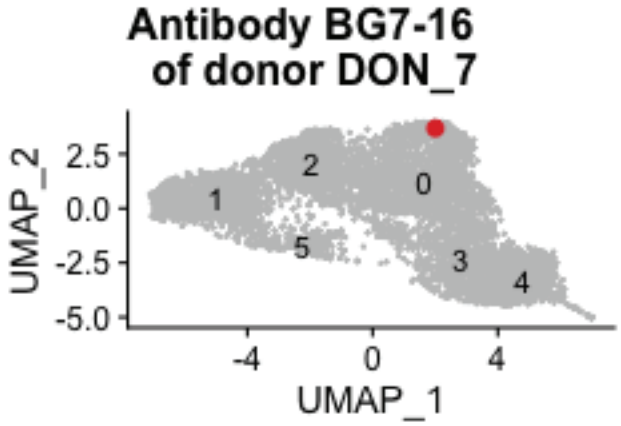
0
1
2
3
4
5


Antibody BG7-16
of donor DON_7
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UMAP_1
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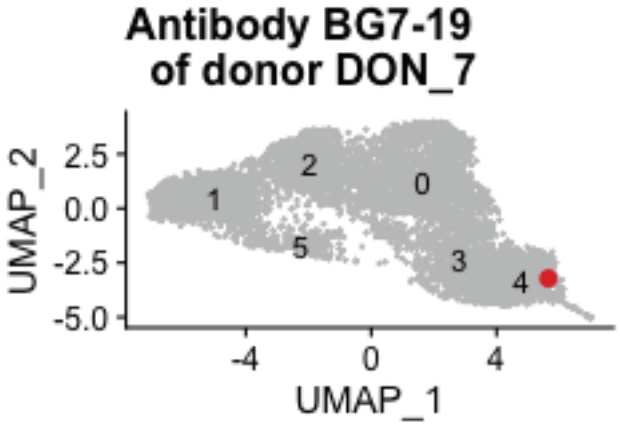
4
5


Antibody BG7-19
of donor DON_7
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1
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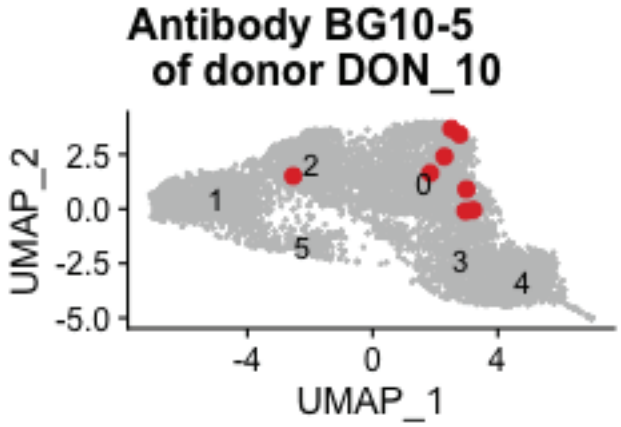
4
5


Antibody BG10-5
of donor DON_10
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UMAP_1
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-5.0
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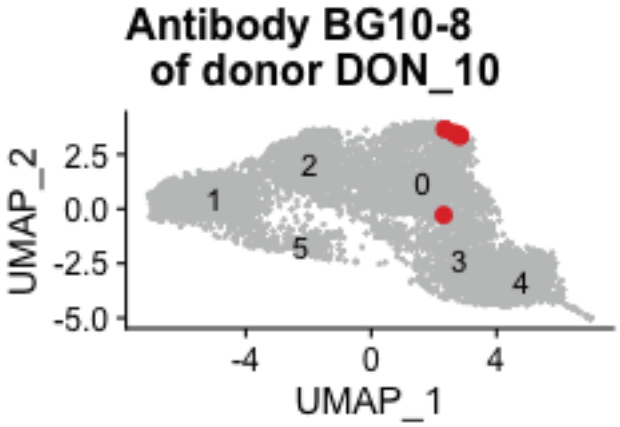
1
2
3
4
5


Antibody BG10-8
of donor DON_10
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UMAP_1
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1
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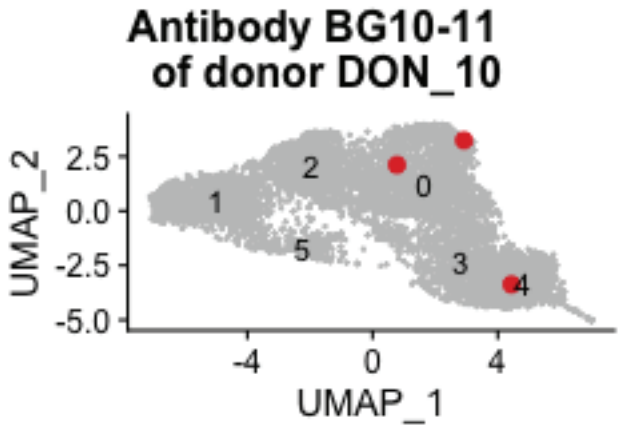
4
5


Antibody BG10-11
of donor DON_10
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UMAP_1
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-2.5
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0
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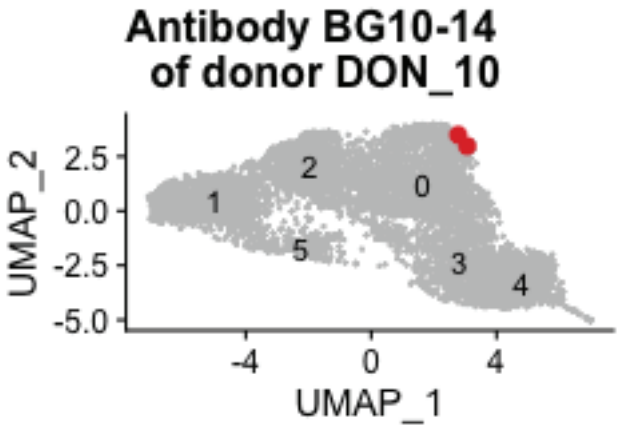
1
2
3
4
5


Antibody BG10-14
of donor DON_10
UMAP_2
UMAP_1
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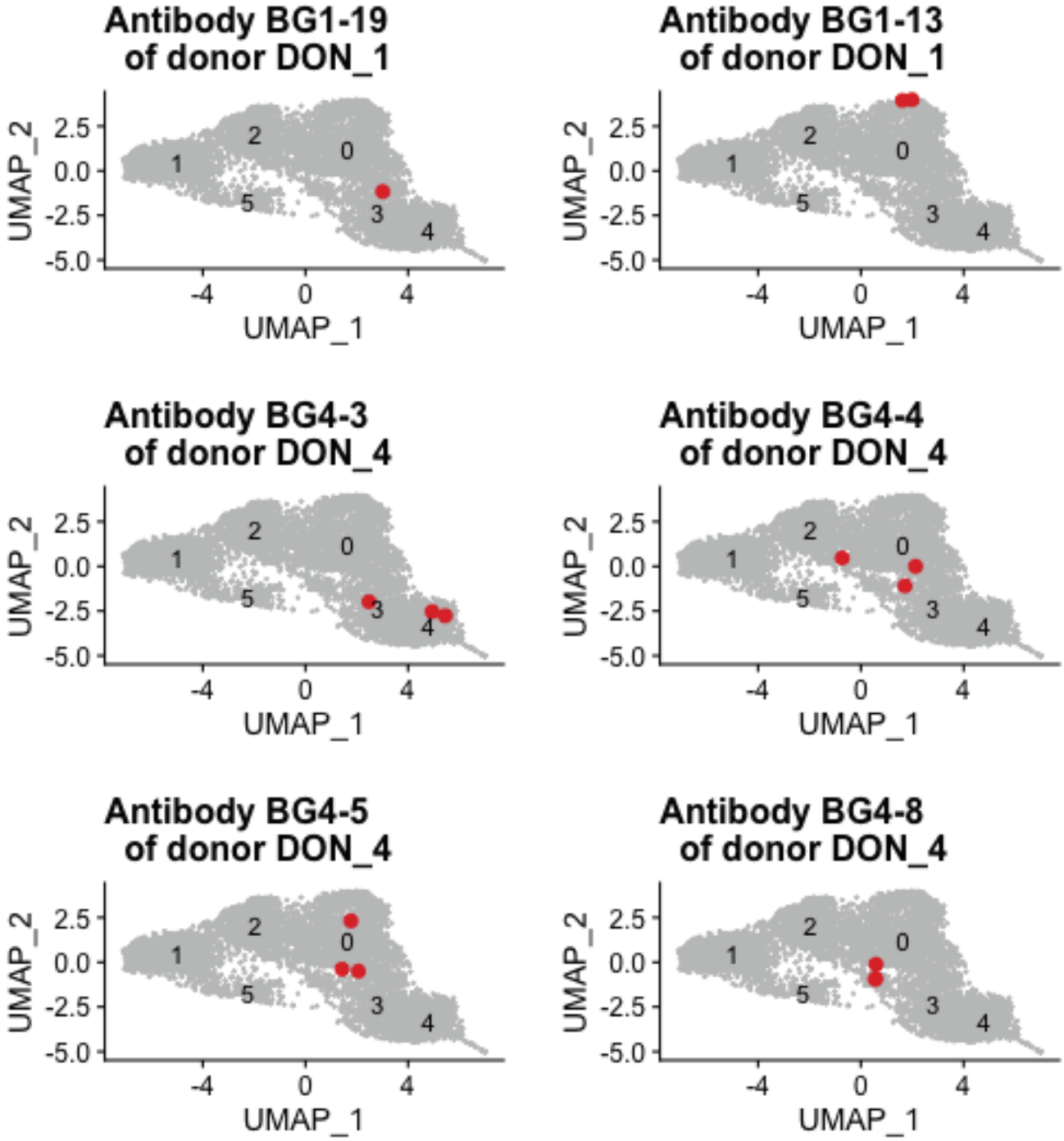
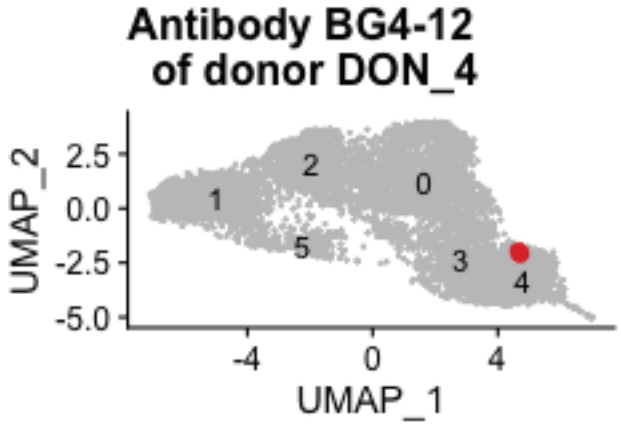
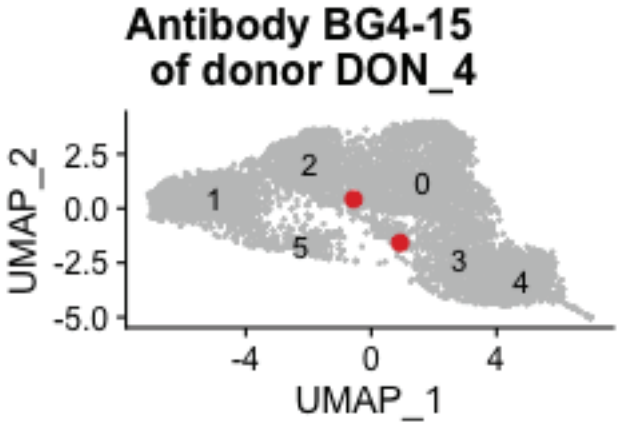
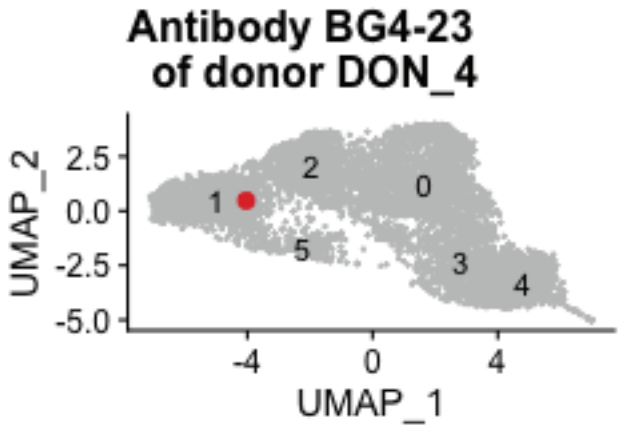
-2.5
-5.0
-4
0
4
0
1
2
3
4
5

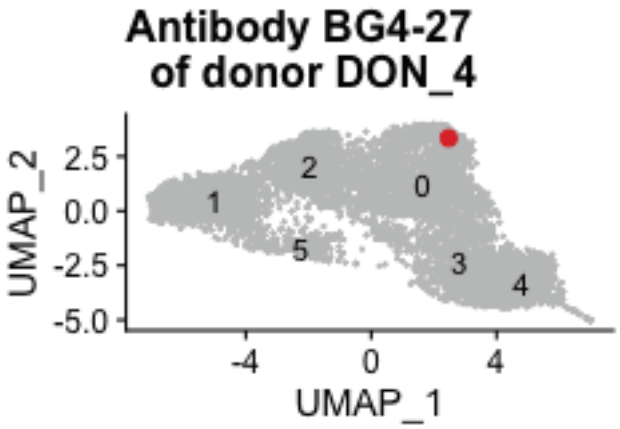
Non-Neutralizing Binding Antibodies



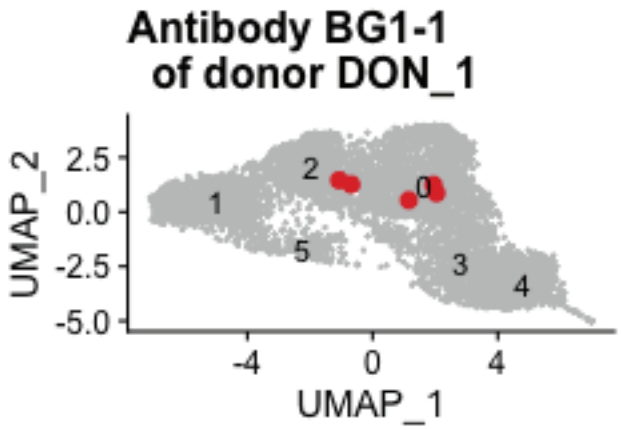


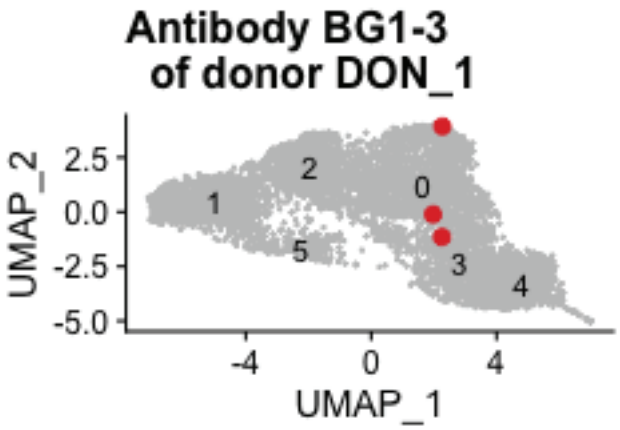


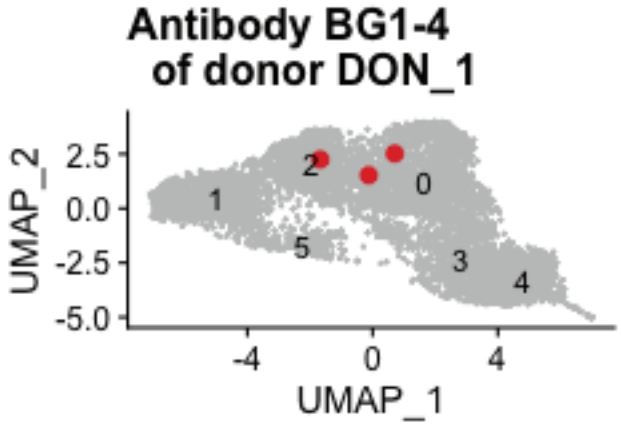


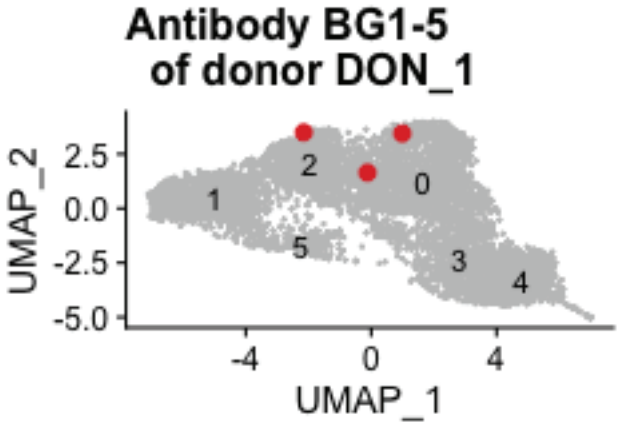


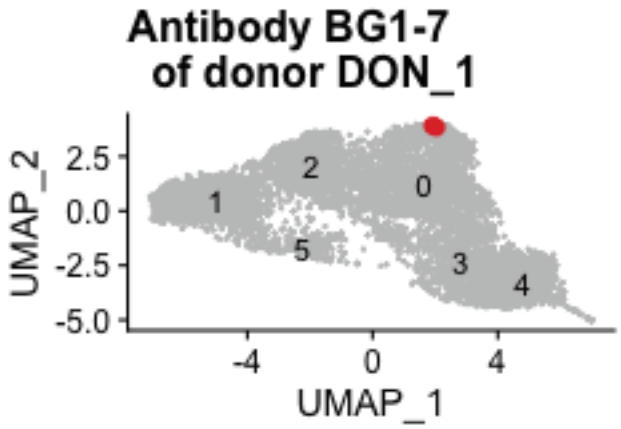
Non-Neutralizing Low-Binding Antibodies

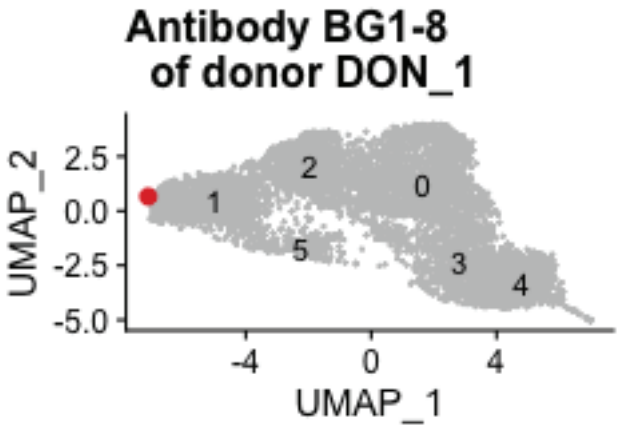





Antibody BG1-4
of donor DON_1
UMAP_2
UMAP_1
2.5
0.0
-2.5
-5.0
-4
0
4
0
1
2
3
4
5


Antibody BG1-5
of donor DON_1
UMAP_2
UMAP_1
2.5
0.0
-2.5
-5.0
-4
0
4
0
1
2
3
4
5


Antibody BG1-7
of donor DON_1
UMAP_2
UMAP_1
2.5
0.0
-2.5
-5.0
-4
0
4
0
1
2
3
4
5


Antibody BG1-8
of donor DON_1
UMAP_2
UMAP_1
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0.0
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-4
0
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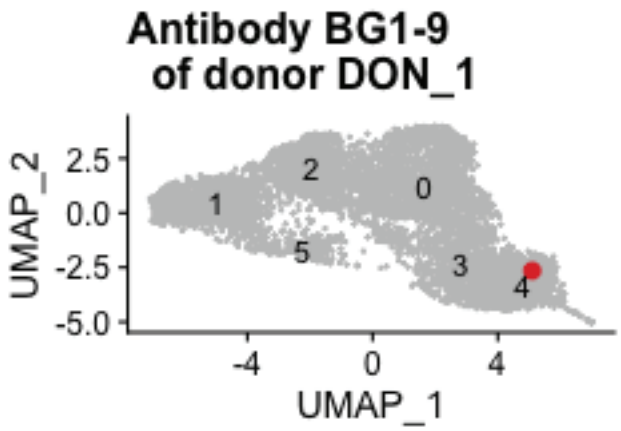
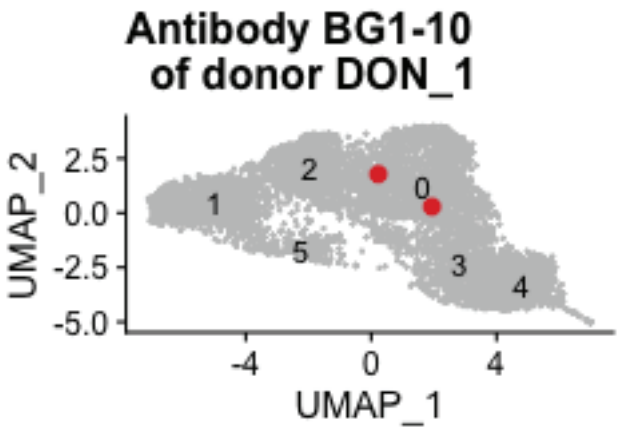
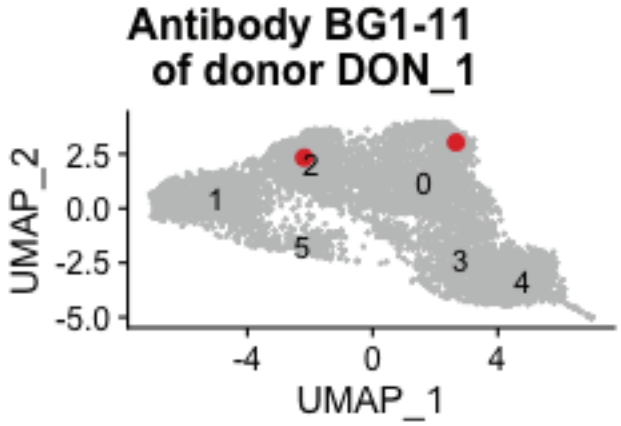
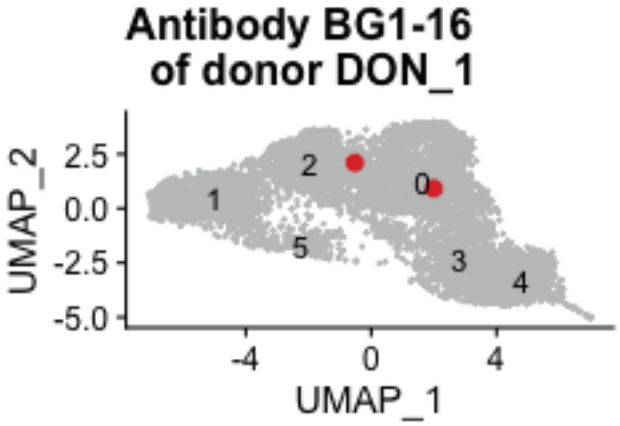
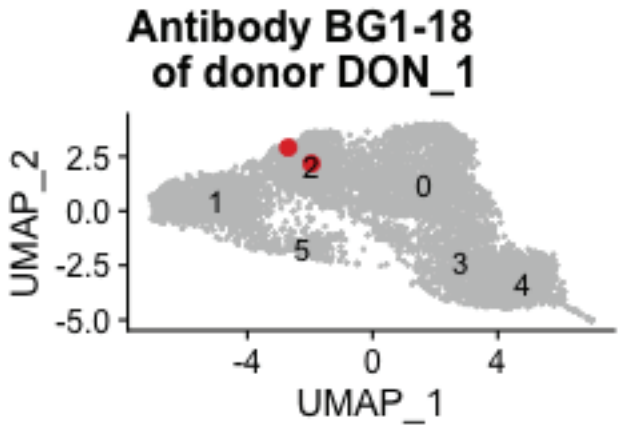
2
3
4
5

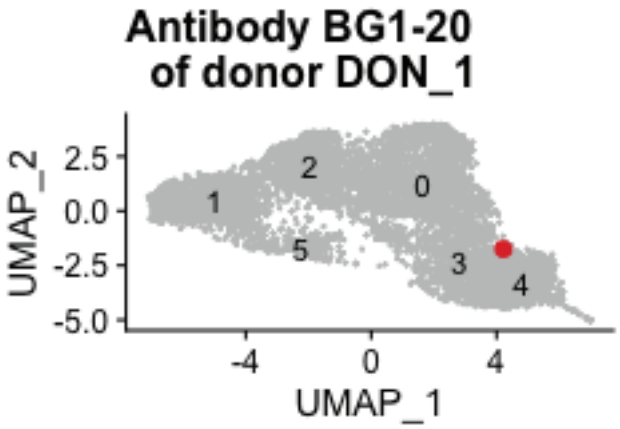

Antibody BG1-9
of donor DON_1
UMAP_2
UMAP_1
2.5
0.0
-2.5
-5.0
-4
0
4
0
1
2
3
4
5

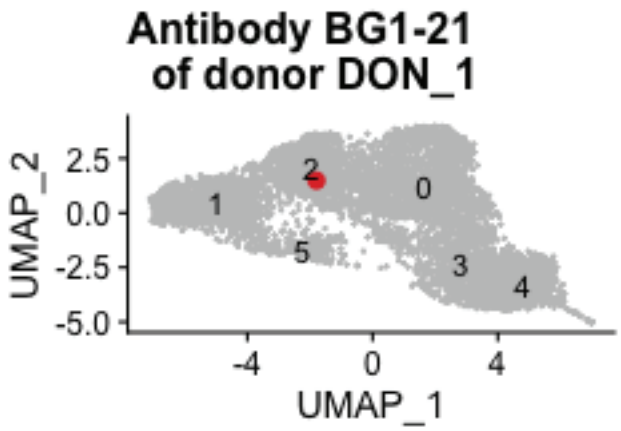

Antibody BG1-10
of donor DON_1
UMAP_2
UMAP_1
2.5
0.0
-2.5
-5.0
-4
0
4
0
1
2
3
4
5

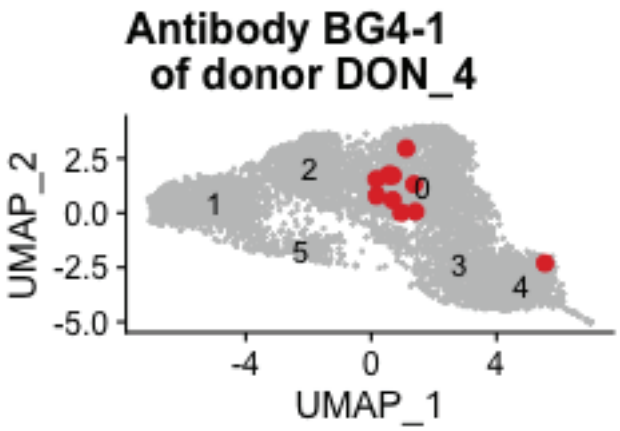

Antibody BG1-11
of donor DON_1
UMAP_2
UMAP_1
2.5
0.0
-2.5
-5.0
-4
0
4
0
1
2
3
4
5

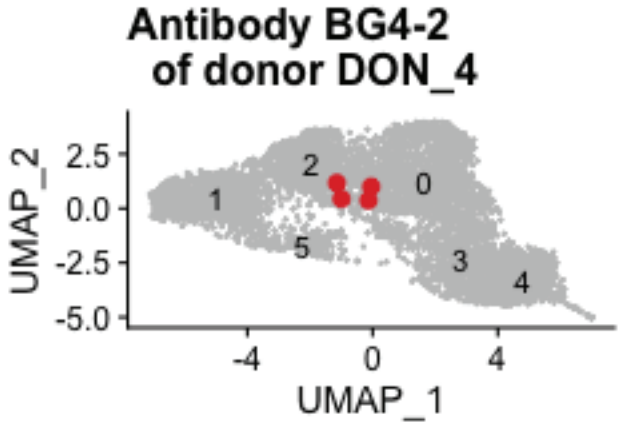

Antibody BG1-16
of donor DON_1
UMAP_2
UMAP_1
2.5
0.0
-2.5
-5.0
-4
0
4
0
1
2
3
4
5

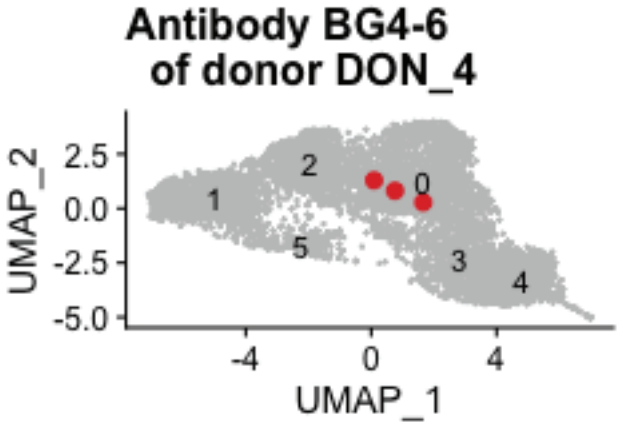

Antibody BG1-18
of donor DON_1
UMAP_2
UMAP_1
2.5
0.0
-2.5
-5.0
-4
0
4
0
1
2
3
4
5

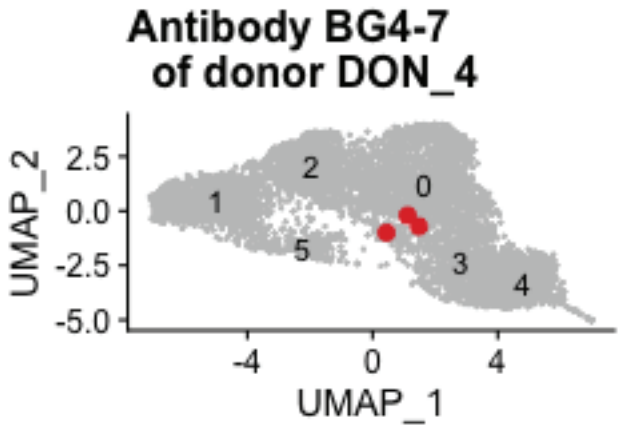

Antibody BG1-20
of donor DON_1
UMAP_2
UMAP_1
2.5
0.0
-2.5
-5.0
-4
0
4
0
1
2
3
4
5

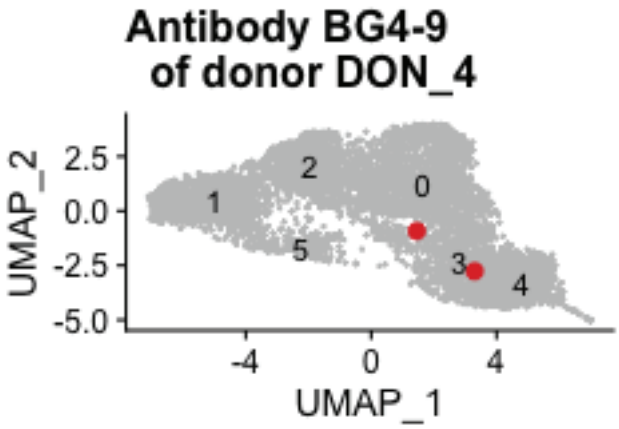

Antibody BG1-21
of donor DON_1
UMAP_2
UMAP_1
2.5
0.0
-2.5
-5.0
-4
0
4
0
1
2
3
4
5

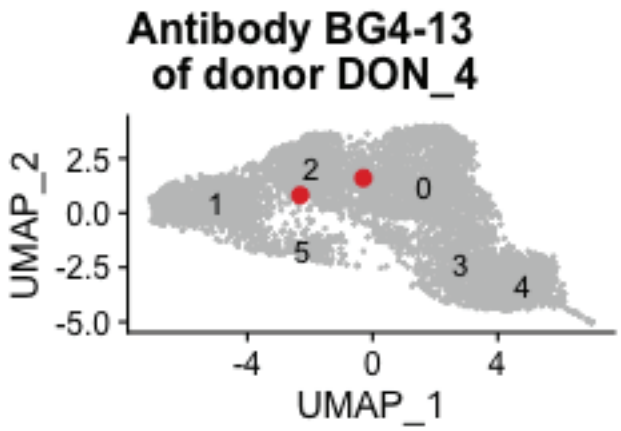

Antibody BG4-1
of donor DON_4
UMAP_2
UMAP_1
2.5
0.0
-2.5
-5.0
-4
0
4
0
1
2
3
4
5

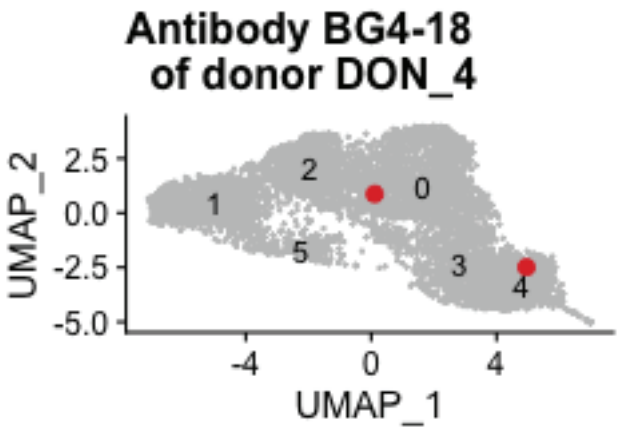

Antibody BG4-2
of donor DON_4
UMAP_2
UMAP_1
2.5
0.0
-2.5
-5.0
-4
0
4
0
1
2
3
4
5


Antibody BG4-6
of donor DON_4
UMAP_2
UMAP_1
2.5
0.0
-2.5
-5.0
-4
0
4
0
1
2
3
4
5


Antibody BG4-7
of donor DON_4
UMAP_2
UMAP_1
2.5
0.0
-2.5
-5.0
-4
0
4
0
1
2
3
4
5


Antibody BG4-9
of donor DON_4
UMAP_2
UMAP_1
2.5
0.0
-2.5
-5.0
-4
0
4
0
1
2
3
4
5


Antibody BG4-13
of donor DON_4
UMAP_2
UMAP_1
2.5
0.0
-2.5
-5.0
-4
0
4
0
1
2
3
4
5


Antibody BG4-18
of donor DON_4
UMAP_2
UMAP_1
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0.0
-2.5
-5.0
-4
0
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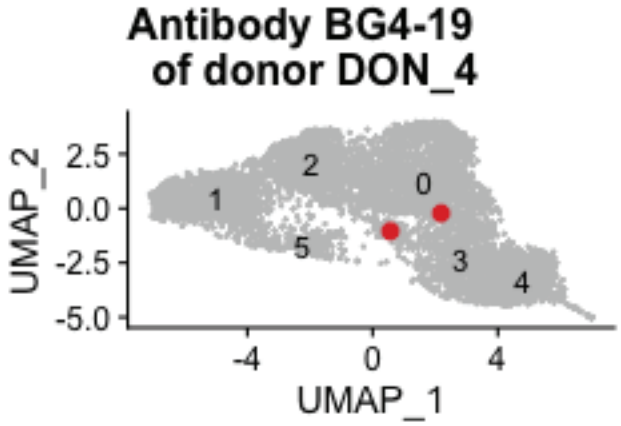
4
5


Antibody BG4-19
of donor DON_4
UMAP_2
UMAP_1
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0.0
-2.5
-5.0
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0
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0
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4
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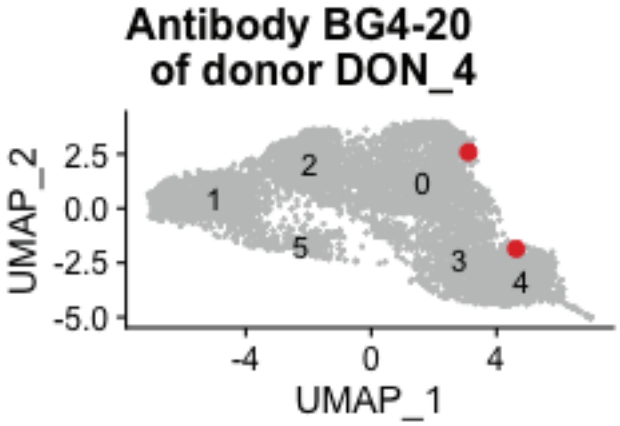
Antibody BG4-20
of donor DON_4
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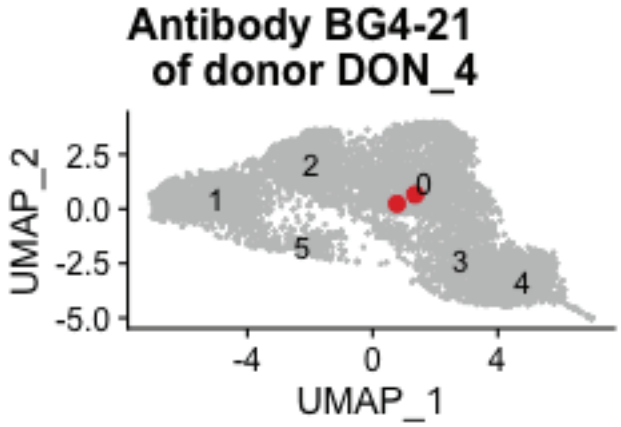
UMAP_1
2.5
0.0
-2.5
-5.0
-4
0
4
0
1
2
3
4
5


Antibody BG4-21
of donor DON_4
UMAP_2
UMAP_1
2.5
0.0
-2.5
-5.0
-4
0
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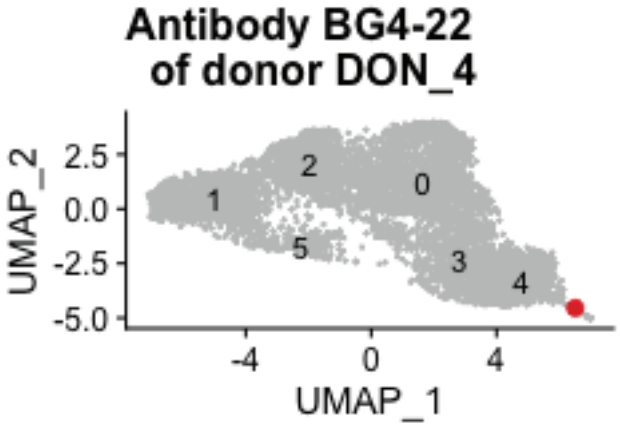
0
1
2
3
4
5


Antibody BG4-22
of donor DON_4
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UMAP_1
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-5.0
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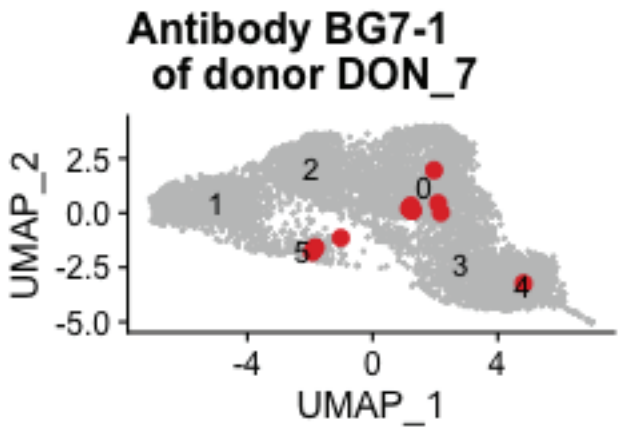
4
5


Antibody BG7-1
of donor DON_7
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UMAP_1
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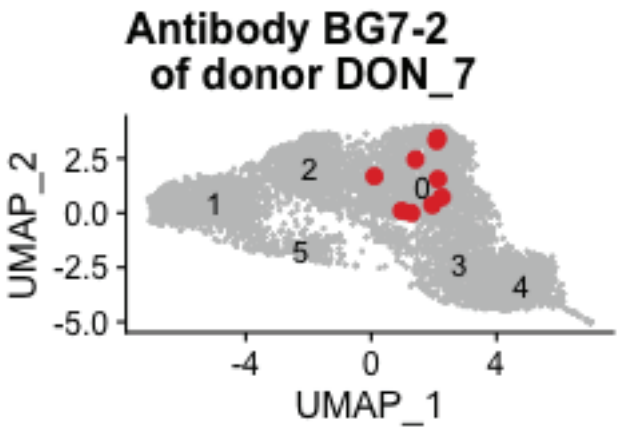
0.0
-2.5
-5.0
-4
0
4
0
1
2
3
4
5


Antibody BG7-2
of donor DON_7
UMAP_2
UMAP_1
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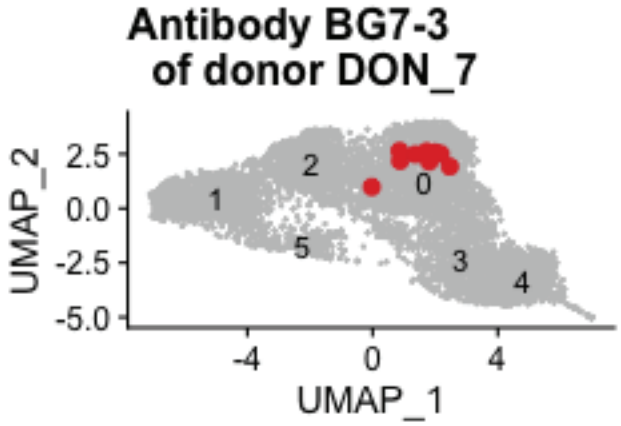
0.0
-2.5
-5.0
-4
0
4
0
1
2
3
4
5


Antibody BG7-3
of donor DON_7
UMAP_2
UMAP_1
2.5
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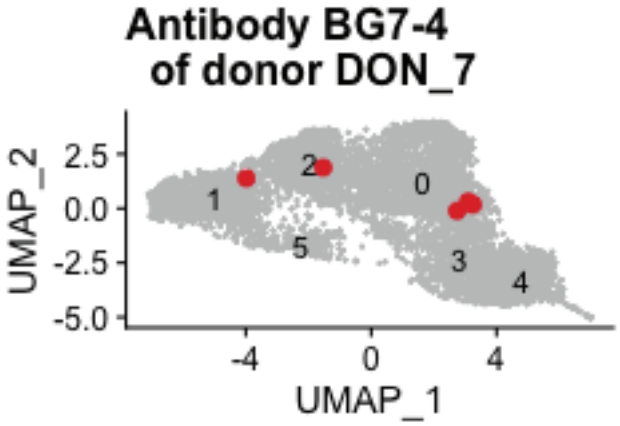
-2.5
-5.0
-4
0
4
0
1
2
3
4
5


Antibody BG7-4
of donor DON_7
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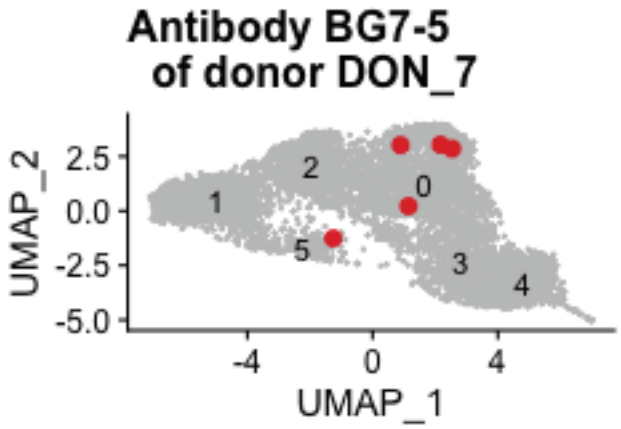
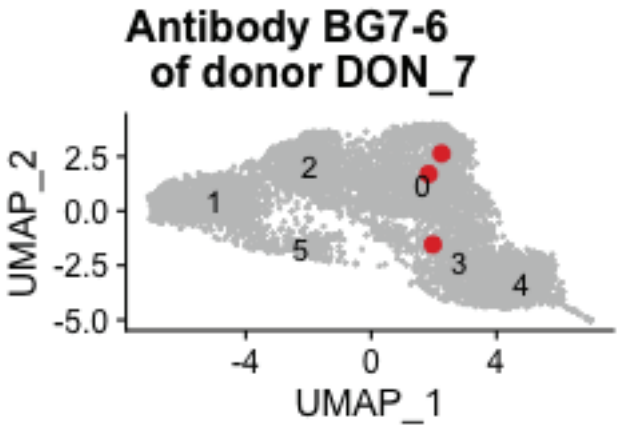
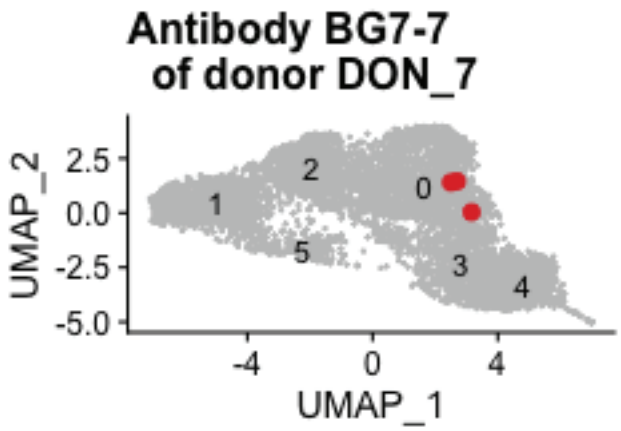
UMAP_1
2.5
0.0
-2.5
-5.0
-4
0
4
0
1
2
3
4
5


Antibody BG7-5
of donor DON_7
UMAP_2
UMAP_1
2.5
0.0
-2.5
-5.0
-4
0
4
0
1
2
3
4
5


Antibody BG7-6
of donor DON_7
UMAP_2
UMAP_1
2.5
0.0
-2.5
-5.0
-4
0
4
0
1
2
3
4
5


Antibody BG7-7
of donor DON_7
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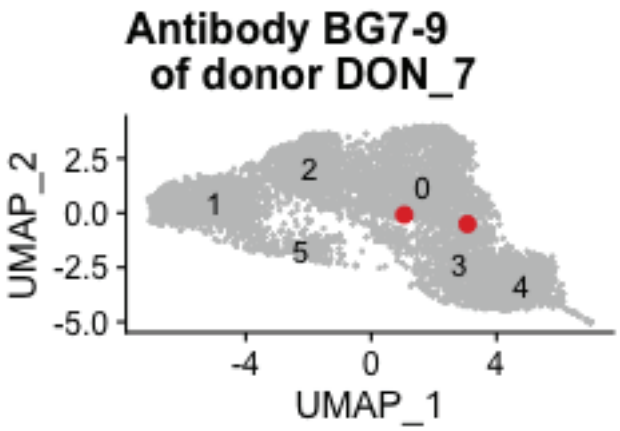
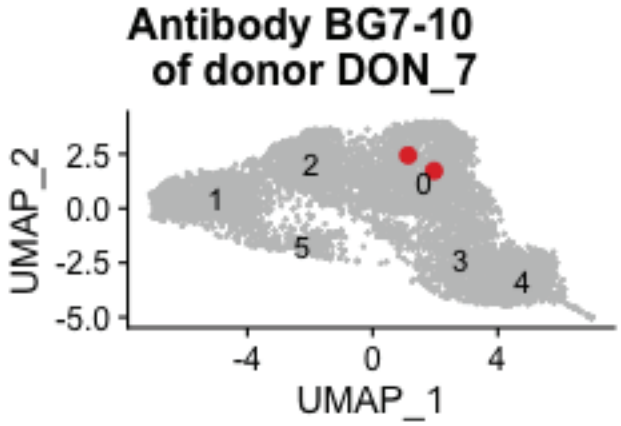
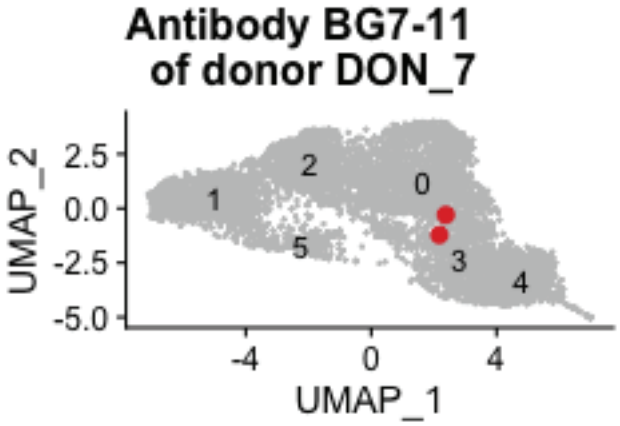
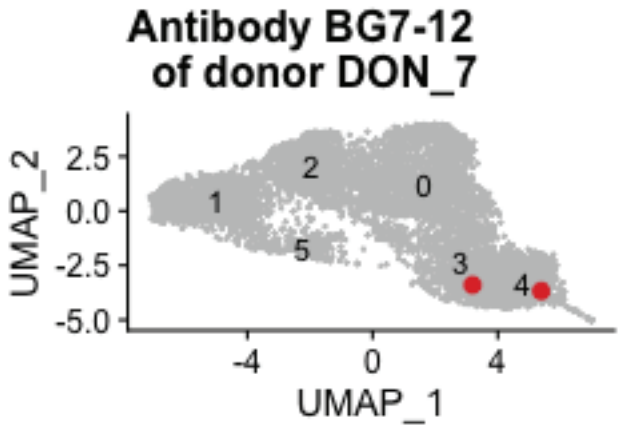
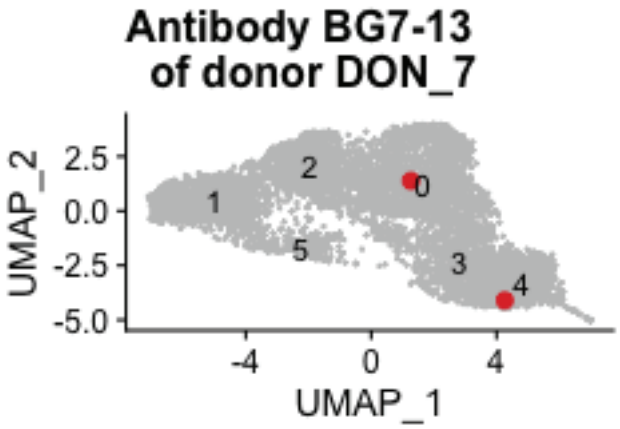
UMAP_1
2.5
0.0
-2.5
-5.0
-4
0
4
0
1
2
3
4
5

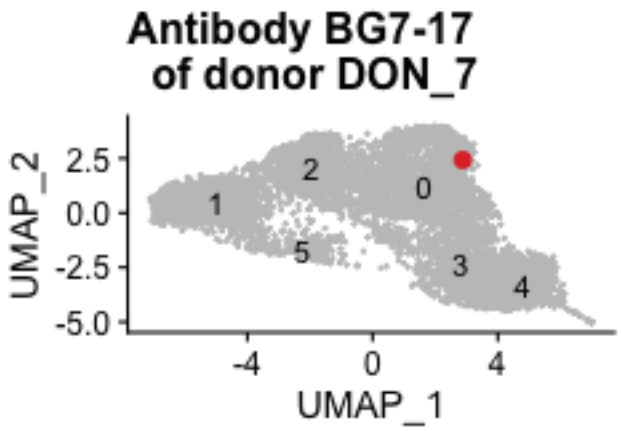

Antibody BG7-9
of donor DON_7
UMAP_2
UMAP_1
2.5
0.0
-2.5
-5.0
-4
0
4
0
1
2
3
4
5

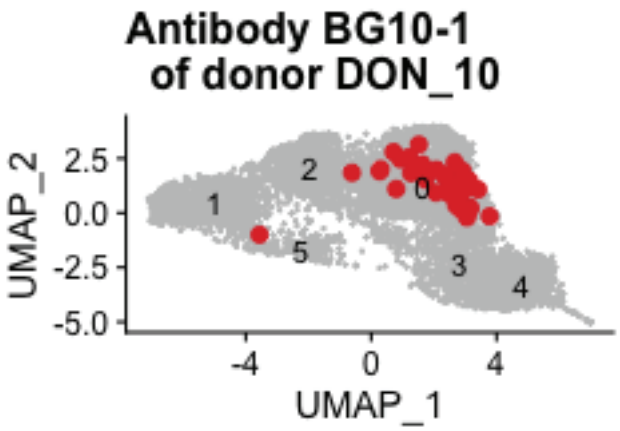

Antibody BG7-10
of donor DON_7
UMAP_2
UMAP_1
2.5
0.0
-2.5
-5.0
-4
0
4
0
1
2
3
4
5

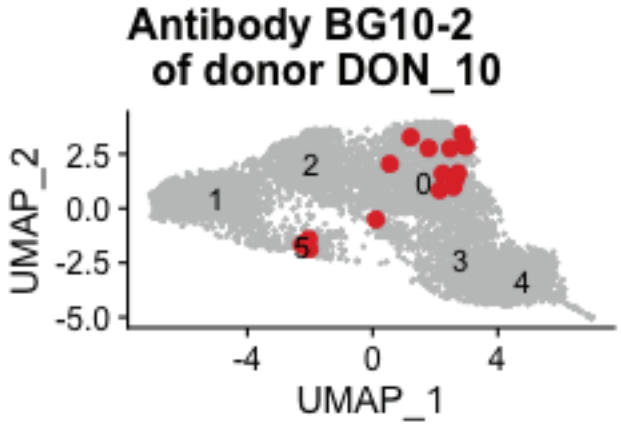

Antibody BG7-11
of donor DON_7
UMAP_2
UMAP_1
2.5
0.0
-2.5
-5.0
-4
0
4
0
1
2
3
4
5

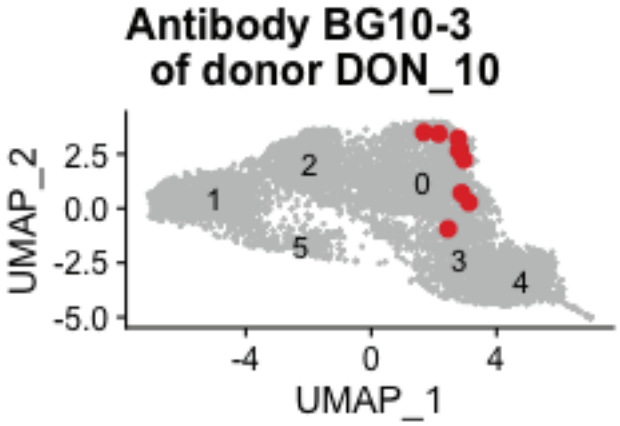

Antibody BG7-12
of donor DON_7
UMAP_2
UMAP_1
2.5
0.0
-2.5
-5.0
-4
0
4
0
1
2
3
4
5

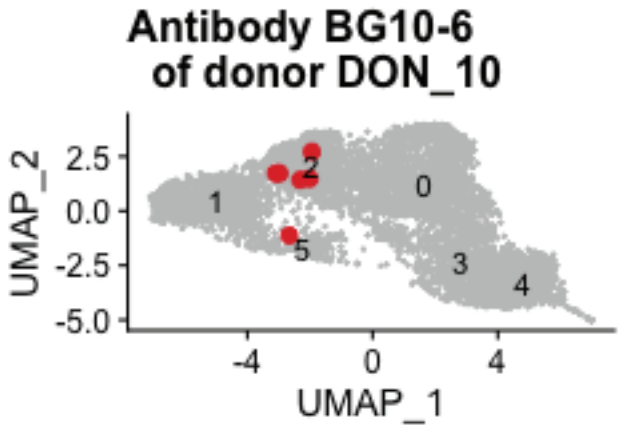

Antibody BG7-13
of donor DON_7
UMAP_2
UMAP_1
2.5
0.0
-2.5
-5.0
-4
0
4
0
1
2
3
4
5

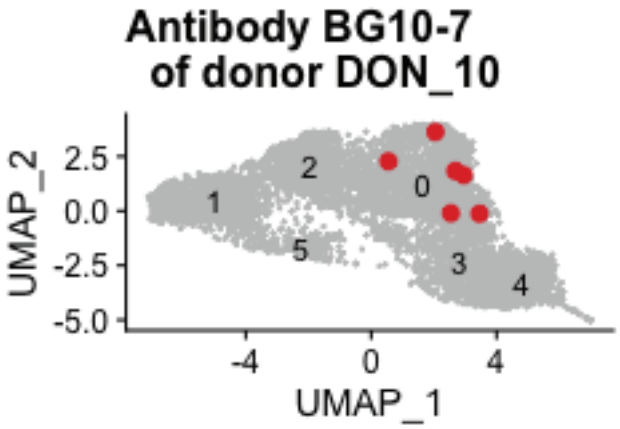

Antibody BG7-17
of donor DON_7
UMAP_2
UMAP_1
2.5
0.0
-2.5
-5.0
-4
0
4
0
1
2
3
4
5

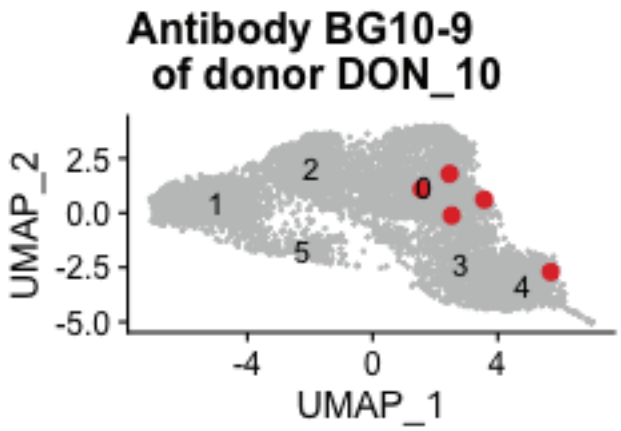

Antibody BG10-1
of donor DON_10
UMAP_2
UMAP_1
2.5
0.0
-2.5
-5.0
-4
0
4
0
1
2
3
4
5

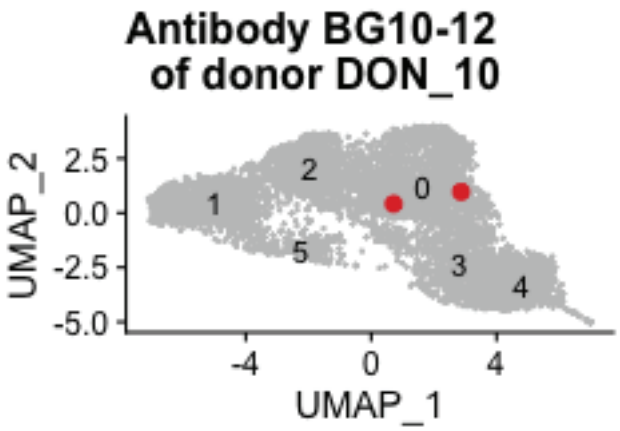

Antibody BG10-2
of donor DON_10
UMAP_2
UMAP_1
2.5
0.0
-2.5
-5.0
-4
0
4
0
1
2
3
4
5

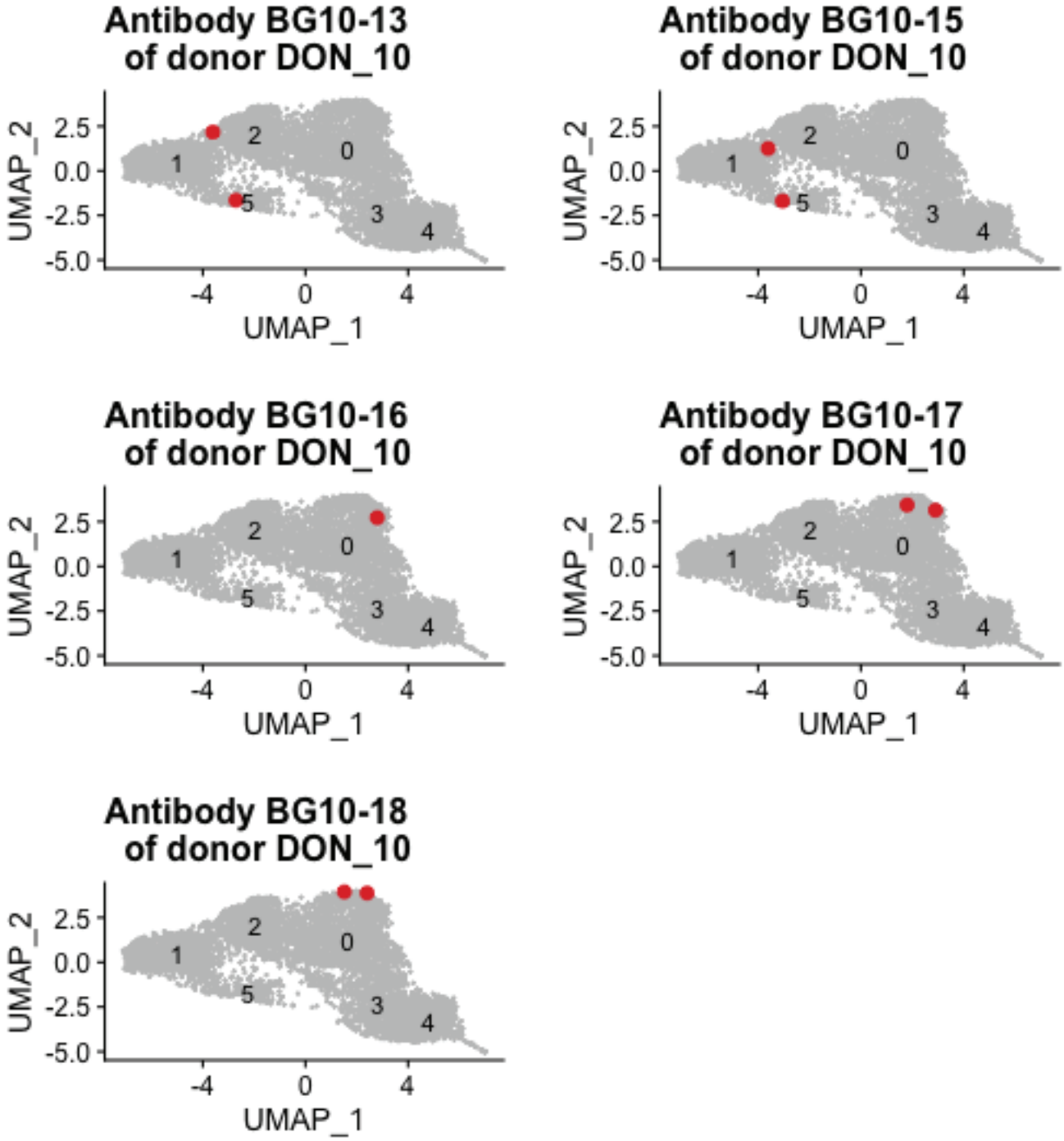

Antibody BG10-3
of donor DON_10
UMAP_2
UMAP_1
2.5
0.0
-2.5
-5.0
-4
0
4
0
1
2
3
4
5


Antibody BG10-6
of donor DON_10
UMAP_2
UMAP_1
2.5
0.0
-2.5
-5.0
-4
0
4
0
1
2
3
4
5


Antibody BG10-7
of donor DON_10
UMAP_2
UMAP_1
2.5
0.0
-2.5
-5.0
-4
0
4
0
1
2
3
4
5


Antibody BG10-9
of donor DON_10
UMAP_2
UMAP_1
2.5
0.0
-2.5
-5.0
-4
0
4
0
1
2
3
4
5


Antibody BG10-12
of donor DON_10
UMAP_2
UMAP_1
2.5
0.0
-2.5
-5.0
-4
0
4
0
1
2
3
4
5



Data S1, Related to Figure 4 and Tables S2 and S3. UMAP plots displaying clonal members of all validated mAbs (Tables S2 and S3). Each plot represents where the tested mAb along with its clonally related cells are mapped on the transcriptome landscape.